

RESULT 2	Db	421 YKSSPEAKMIRPCKFKEP 439	C; Genetics: must:blp C; Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology F; 203-428/Domain: fibrinogen beta/gamma homology <FBG>
A27447			
cytotoxic T-lymphocyte-specific protein precursor (clone pT45) - mouse			
C; Species: Mus musculus (house mouse)			
C; Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1993			
C; Accession: A27447			
R; Kobama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H.			
Proc. Natl. Acad. Sci. U.S.A. 84: 1609-1613, 1987			
A; Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to			
A; Reference number: A27447; MUID:87175527; PMID:3550794			
A; Accession: A27447			
A; Molecule type: mRNA			
A; Residues: 1-432 <KCY>			
A; Cross-references: GB:M16238; NID:913304; PMID:AAA37624.1; PID:9387156			
C; Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology <FBG>			
F; 203-428/Domain: fibrinogen beta/gamma homology <FBG>			
Query Match 77.9% Score 1853.5 DB 2 Length 432;			
Best Local Similarity 77.7% Pred. No. 8.1e-121; Mismatches 42; Indels 7; Gaps 4;			
Matches 340; Conservative 42; MisMatches 50; Indels 7; Gaps 4;			
Qy 1 MKLANKWYISSLSSAVIATYGFIVANNSTEIKEKDKVCPVLESRGKCEAGECPYQVS 60			
Db 1 MRLPGLWLSSAVLAACR-AVEEHNLTTEGLEDASQAACPARLESGRC-EGSQCPFPQT 58			
Qy 61 IPIPTICLKPKSRIEEVFENQNLKE-VNLURKSQQDCLQADQNGDPRNGLLPSTG 120			
Db 59 IPIPTICLKPKSRIEEVFENQNLKE-VNLURKSQQDCLQADQNGDPRNGLLPSTG 120			
Qy 121 APGEVGDNVRVLESEYNKLSELKSLKAEVLEIINVHLGRLEKUNLVNNNNNNYVDVKVANL 180			
Db 115 AE-TAEDSRVQELESQYNLKSELKSLKAEVLEIINVHLGRLEKUNLVNNNNNNYVDVKVANL 174			
Qy 161 FVVNSLDGKSKCPSPQEQIOSRPVPOHLYKDCSYAAIGKRSSETYRVTPDKNNSSEV 240			
Db 174 FVVNSLDGKSKCPSPQEQIOSRPVPOHLYKDCSYAAIGKRSSETYRVTPDKNNSSEV 233			
Qy 241 YCDMETMGGMGTWVQASLDGSTNFETWDQYKAGEFNLRREFWLGNDKHLTKSKEMIL 300			
Db 234 YCDMETMGGMGTWVQASLDGSTNFETWDQYKAGEFNLRREFWLGNDKHLTKSKEMIL 293			
Qy 301 RIDLEDENGVELYALYQOFYANEFLKYRLHVGNNGTAGDAFLRNKHYNHDLKPFPTPC 360			
Db 294 RIDLEDENGVLTYALYQOFYANEFLKYRLHVGNNGTAGDAFLRNKHYNHDLKPFPTPD 353			
Qy 365 KDNDRYPSNCGQLYYSSQWKFACLSANLNGKYYHKYKYGVRNGFWGTMGPVSBAHPGG 420			
Db 354 RDNDRYPSNCGQLYYSSQWKFACLSANLNGKYYHKYKYGVRNGFWGTMGPVSBAHPGG 413			
Qy 421 YKSSPEAKMIRPCKFKEP 439			
Db 414 YKSSPEAKMIRPCKFKEP 432			
RESULT 4			
YCDMETMGGMGTWVQASLDGSTNFETWDQYKAGEFNLRREFWLGNDKHLTKSKEMIL 300			
234 YCDMETMGGMGTWVQASLDGSTNFETWDQYKAGEFNLRREFWLGNDKHLTKSKEMIL 293			
Qy 301 RIDLEDENGVELYALYQOFYANEFLKYRLHVGNNGTAGDAFLRNKHYNHDLKPFPTD 360			
Db 294 RIDLEDENGVLTYALYQOFYANEFLKYRLHVGNNGTAGDAFLRNKHYNHDLKPFPTD 353			
Qy 361 KDNDRYPSNCGQLYYSSQWKFACLSANLNGKYYHKYKYGVRNGFWGTMGPVSBAHPGG 420			
Db 354 RDNDRYPSNCGQLYYSSQWKFACLSANLNGKYYHKYKYGVRNGFWGTMGPVSBAHPGG 413			
Qy 421 YKSSPEAKMIRPCKFKEP 439			
Db 414 YKSSPEAKMIRPCKFKEP 432			
RESULT 3			
fibrinogen-like protein - mouse			
C; Species: Mus sp. (mouse)			
C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999			
R; Parr, R.L.; Fung, L.; Reineker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.			
J. Virol. 69: 5033-5038, 1995			
A; Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induce			
A; Reference number: 156594; PMID:9533285; PMID:7609373			
A; Accession: 156594			
A; Molecule type: mRNA			
A; Residues: 1-332 <RES>			
A; Cross-references: GB:AB34923.1; PMID:91042169; PMID:AB34923.1; PMID:91042170			
Qy 85 -----LKEIINSLIKS-QDCDKLQADQNGDPRNGLLPSTGAPGEUDNRNVRLE 134			
Db 138 VAKFSDTSTTMQYVNM-DNKLVKTQKQRKD-----NDTSEYNTMELHYNIK-D 159			

RESULT 5
JN0596
fibrinogen-related protein HFREP-1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: JN0596
R;Amamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Bioscat. Biophys. Res. Commun. 193, 681-687, 1993
A;Title: Molecular cloning and initial characterization of a novel fibrinogen-related gene
A;Reference number: CNU0596
A;Accession: CNU0596
A;Molecule type: mRNA
A;Residues: 1-312 <YAM>
A;Cross-references: GB:D:4446; NID:9393314; PID:BAAC3316.i; PID:9393315
A;Experimental source: liver
A;Family: fibrinogen beta/gamma homology
F;1-17/Domain: signal sequence #status Predicted <SIG>
F;18-312/Product: fibrinogen-related protein HFREP-1 #status Predicted <MAT>
F;80-305/Domain: fibrinogen: beta/gamma homology <FBG>

Query Match
Best Local Similarity 36.8%; Score 506.51; DB: 2; Length 312;
Matches 218; Conservative 38; Mismatches 06; Index 57; Gaps 2;

Qy 129 RYRELESEYNKLSSEIYNAKEFEINLHGRLEKINLYNNMANNENYYDSKVANITFYVNSLD 188
Db 36 QVRLEIETRKQQYKIKQLQE ----- New QFLRGDETVVD ----- 73

Qy 189 GKCSKCPSEQIQSRPVQHUYKDCSDYYAIGKASSETYRTPDPKNSSEPVYCDMETS 248
Db 74 -----LGSKRQ-----YADCYEFLNDGKYLGSFYK-KPLOSPAEVSYCDNSD-G 117

Qy 249 GWIV-QAEDGSINFTRWQDAGSFNL--REPPFGNKRHLITKSEMINRIDE 305
Db 118 GWTWVQRSQSGSENFRNCWDYENGFSNVQKGEWLNQKNNLHEUTTCBQYKLIDLA 177

Qy 306 DENGVELAYDQFYVANEFLKYR-HGVNYNGTAGDALRFNKH-----YNHD-KPFTT? 359
Db 178 DEFKNSRYAQYRNPKVGDFKRNPEJNGETYSAGDSLGNRHPETJWASHQRKFSTW 237

Qy 360 DKNDRYPGSGCGLYSSGWEDACLSANLNQSKYHQKYRG-VRNQIFACTPGYSEAHP 418
Db 238 DRDIDH-B-CGCAEDBEDQWNRCHSAANLGYVYSGPY-ZARTDNGWVTTW----- 288

Qy 419 GYKSSFKRARMERPRPKP 439
Db 289 HGWWSLKSVMKIRNDTP 309

RESULT 6
EGFBG
fibrinogen Gamma-B chain precursor [validated] - human
N;Alternate names: coagulation factor I; fibrinogen gamma-5S chain
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence 17-Mar-1987 #text_change 06-Dec-2003
C;Accession: A90194; A92448; A90453; A22203; B2303; I37390; AC126
R;Lixton, M.W.; Chuns, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A;Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A;Accession number: A90194; MUID:85252774; PMID:2390550
A;Molecule type: DNA
A;Residues: 1-113; T, 115-453 <RIX>
A;Cross-references: GB:M0014; GB:J00134; GB:J00135; GB:X00086; NID:9182438; PID:AA85
R;Porter Jr., A.C.; Cummings, D.E.; Crabb, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A;Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A;Accession number: A92448; MUID:85030379; PMID:6092346
A;Molecule type: DNA
A;Residues: 286-453 <FOR>
R;Wolfenstein-Todel, C.; Mcesson, M.W.
Biochemistry 20, 6146-6149, 1981
A;Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A;Accession: A90453; MUID:82068933; PMID:7306501
A;Molecule type: Protein
A;Residues: 411-434 'Y', 436-440 'Z', 442 'Z', 444 'B', 446-447 'R', 449 'ZBB' , 453 <WCL>
A;Cross-references: 411-434 'Y', 436-440 'Z', 442 'Z', 444 'B', 446-447 'R', 449 'ZBB' , 453 <WCL>
R;Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A;Title: Carboxy-terminal amino acid sequences of two variant forms of the gamma-chain
A;Accession number: A94194; MUID:88217900; PMID:3368448
A;Molecule type: Protein
A;Residues: 433-449 <FR4>
A;Accession: A90453
A;Molecule type: Protein
A;Residues: 433-453 <FR2>
R;Marchetti, L.; Zarelli, M.; Valcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A;Title: Polymorphism of the human gamma chain fibrinogen gene.
A;Accession number: 137390; MUID:92119334; PMID:1685103
A;Accession: 137390
A;Description: The gamma-B chain is present in about 10% of the fibrinogen molecules in platelets.
A;Molecule type: mRNA
A;Accession: B2623
A;Molecule type: Protein
A;Residues: 433-453 <FR2>
R;Marchetti, L.; Zarelli, M.; Valcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A;Title: Polymorphism of the human gamma chain fibrinogen gene.
A;Accession number: 137390; MUID:92119334; PMID:1685103
A;Accession: 137390
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Keywords: fibrinogen gamma chain; fibrinogen beta/gamma homology
C;Cross-references: EMBL:X51473; NID:931410; PID:CAA35837.1; P2D:G93C064
A;XNP Position: 4928-4928
A;Introns: 41/3; 103/1; 134/2; 175/1; 222/3; 284/2; 377/1
C;Comment: The two forms of Gamma chain A (see PIR:FRUG) and B, arise by alternative splicing, which makes this chain different from the Gamma-B chain at positions 434-437 and 438-439. The Gamma-B chain is contained in about 10% of the fibrinogen molecules in platelets.
C;Genetics:
A;Gene: G3B_FCG
A;Cross-references: EMBL:119132; OMIM:134350
A;XNP Position: 4928-4928
A;Introns: 41/3; 103/1; 134/2; 175/1; 222/3; 284/2; 377/1
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FRUG) chains are contained in the core. Two three-chain coiled coils emerge from this core and form the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Keywords: fibrinogen gamma chain; fibrinogen beta/gamma homology
C;Cross-references: EMBL:119132; OMIM:134350
A;XNP Position: 4928-4928
A;Introns: 41/3; 103/1; 134/2; 175/1; 222/3; 284/2; 377/1
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FRUG) chains are contained in the core. Two three-chain coiled coils emerge from this core and form the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Keywords: fibrinogen gamma chain; fibrinogen beta/gamma homology
C;Cross-references: EMBL:119132; OMIM:134350
A;XNP Position: 4928-4928
A;Introns: 41/3; 103/1; 134/2; 175/1; 222/3; 284/2; 377/1
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FRUG) chains are contained in the core. Two three-chain coiled coils emerge from this core and form the distal domain nodes.

F;49/D-sulfide bonds: interchain (to alpha-64) #status predicted
 F;78/B-binding site: carbohydrate (Asn) (covalent) #status predicted
 F;161/Disulfide bonds: interchain (to beta-227) #status predicted
 F;165/Disulfide bonds: interchain (to alpha-190) #status predicted
 F;179-358,352-365/Disulfide bonds: #status predicted
 F;224/Cross-link: isopeptide (Gln)
 F;432/Cross-link: isopeptide (Lys)
 F;432/Cross-link: isopeptide (Lys) (interchain to Gln-124) #status predicted
 F;432/Cross-link: isopeptide (Lys) (interchain to Gln-124) #status predicted

Query Match Score 484.5; DB 1; length 453;
 Best Local Similarity 29.7%; Pred. No. 5.5e-26;
 Matches 141; Conservative 56; Mismatches 178; Inels 99; Gaps 18;

Qy 8 WLSAVLAVYGFVWANNETEIKDERAKVCPVRLSERGKCEEA3CPCQVNSL2FLTIQ 67
 Db 19 FSSTCVA----YVATRNCCLDERFGSYCF----TGTIAFLSFLSYGTX 61
 Qy 68 LPKQFSRIEVEFKEVONLKEITINSLKSQCCDKLQADDNGDGRGNGLUFLSTGAPEVGQ 127
 Db 62 VDKDQLOSLELHVNENKTSEVKOLIKAIQ-LTYNPKQSKPNMI-----DAAT 109
 Qy 128 NRYFELASPVKLUSSLNAAKNEAVNLHGRLEKLYDMMKENVDSKVNNTIVFVNL 187
 Db 110 LKSKRMKLEIINKYEASILTTHCSIRYLQ----EYNSNN----OKTINLKEKVAQL 157
 Qy 188 DGKCSKCKPQEQQTSRSPQHLIYRDCSDYIAKGKRSSETYRTPDPRQNSSPPEVYCEMETN 247
 Db 158 EACQG----PCKDTIQ----IHDITQKGDCOPIANAKQGJYFPLKRNQGQJYVYEDGS 213
 Qy 248 GGGNTVQLARDGSTKTFRTWDQYKAGFGLN----REFEWLQNDKHLTKSKEM----ZLR 301
 Db 214 GNGATVFGQRDGSDFQKRNQIQRREGQHLSPTGTGFWLNEKHLISTQSAYIYAJR 273
 Qy 332 TLEDFENGFLWYLYDQFVYANEFLKSYLHGNY-NKTAKBL-RENKHYTDKJKEFT-- 357
 Db 274 VELEDWNGTSTAYAMFNGPDEADKYLTAFAFGDAGDFDGFQGDFSDKEFTSH 333
 Cy 358 ----T2PKDNDEYPSGNGLYNSSGKWFDAUJSANXNGKYH----QKFRGVRNG 464
 Db 334 NGMCFSTKNDNCF-EGNCAEQGQWYKMKHAGHNGUYQGETYSKASTNEYDNG 392
 Qy 405 TFKGWP----GVSEA--HPGQYKSSFKEARMMIRPKH 436
 Db 393 ZIATWKTRWYSKKTTMKIIPPNRLLTIGEGQHHLGAK----QVREEH 438

RESULT 7
 fibrinogen gamma-A chain precursor (validated) - human
 N:Alternative names: coagulation factor 2
 C:Accession: A90470; B0494; C94433; B93956; B32448; I37593; A40658; H54223; A03125; C37
 C:Date: 24-Apr-1984 #sequence revision 25-Feb-1985 #text change 08-Dec-2000
 R;Crung, D.W.; Chan, W.Y.; Davie, E.W.
 Biochemistry 22, 3250-3256, 1983
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for the gamma
 A:Reference number: A90470; MUID:83283434; PMID:6688357
 A:Accession: A90470
 A:Molecule type: mRNA
 A:Accessories: 1-437 CHU
 R;Rixon, M.W.; Chang, D.W.; Davie, E.W.
 Biochemistry 24, 2077-2086, 1985
 A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
 A:Reference number: A90194; MUID:2990550

A:Accession: A90494
 A:Molecule type: DNA
 A:Residues: 1-113, 1',115-437 <R_X>; PID:AB59531.1; PMID:9182439
 A:Cross-references: GB:X02415; GB:MI014; NID:gi:82438; PID:AB59531.1; PMID:9182439
 R;Henschel, A.; Lottspeich, F.; Schutten, C.; Topfer-Petersen, E.
 in Proteins of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56.
 A:Reference number: A90C6; MUID:85014892; PMID:6592597
 A:Contents: annotation: polymerization site within segment Thr-3
 R;Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.
 Biochemistry 23, 1767-1774, 1994

Qy	259	DGSTNFRTWQDYKAGFGNLR-----REFMLGNDKIKIILITSKEMIRLRLDEDF	307	Best local similarity 30.6%; Pred. No. 5.8e-25;
Db	278	DGSSENFARDWNTYKAEGNIAFGNGKSICNIPGEYLGTKTVHQLTKHTCQVLFDMSDK	337	Matches 129; Conservative 57; Mismatches 149; Indels 86; Gaps 13;
Qy	306	NGVELYALYDQFYVANEFLKYRHLVNEYNGTAGKYY-----RFNKHYN-HD-LKEFTT	358	Gy 61 LPPLTICLKPQFSRIE-VFKEVKON-KEIVVNLKKSCQDC--KLOADDNGDPGRNGLLIP 1-17
Db	338	BESSVTAQAYASSPRPENAAQYRLWVEDYSGRAGNALLEGATQLMGNRMTINHGQFST	397	Db 82 LCTGCKLQLDTLVRQERPIRKIEDRNTVOSVRSSTSSTQYITLKKNNMKGR-----135
Qy	359	PRKDNDRY----PSGNCGLYSSGWRFDACLSANLNGKYY-----HOKYRGVYNGIFW	407	Qy 118 STGARPEVGDNPVRELESEVNKLSELKNAKEEINVLHGLEKLNLYVNMANIENYVDISKV 177
Qy	398	FDRDNDWNPGGPTKHLSREDDGGWYNRCHAANPNGRYWGTYKEQADYGDDGVW	457	Db 119 STGARPEVGDNPVRELESEVNKLSELKNAKEEINVLHGLEKLNLYVNMANIENYVDISKV 177
Qy	408	GTWPQVSEAHAPPQGYKSSFKEXAMMTRPK	415	Db 120 STGARPEVGDNPVRELESEVNKLSELKNAKEEINVLHGLEKLNLYVNMANIENYVDISKV 177
Db	458	MWKG-----SWY--SYRQNMKLRPK	477	Db 121 STGARPEVGDNPVRELESEVNKLSELKNAKEEINVLHGLEKLNLYVNMANIENYVDISKV 177
RESULt 9				
FGBOB				
N; Contains: fibrinopeptide B				
C; Species: Bos primigenius taurus (cattle)				
C; Date: 9-Jul-1981 #sequence revision on 29-Jul-1981 #text_change 13-Sep-1995				
C; Accession: A03122; BC3111; B37507; A37513; S02443				
R; Blobback, B.; Doolittle, R.F.				
Acta Chem. Scand. 17, 1816-1819, 1963				
A; Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.				
A; Reference number: A03122				
A; Molecule type: protein				
R; Sjogrist, J.; Blobback, B.; Malich, P.				
Ark. Kemi 16, 425-436, 1963				
A; Title: Amino acid sequence of bovine fibrinopeptides.				
A; Reference number: AC3117				
A; Accession: B03117				RESULT 10
A; Molecule type: protein				
A; Residues: 5-21 <SJO>				
R; Martinelli, R.A.; Inglis, A.S.; Robira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Jeach, S.				
Arch. Biochem. Biophys. 192, 27-32, 1979				
A; Title: Amino acid sequences of positions of the alpha and beta chains of bovine fibrinopeptides.				
A; Reference number: A73507; MJID:79164394; PXD:434821				
A; Accession: B37507				
A; Molecule type: protein				
A; Residues: 22-53 <MAR>				
R; Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.				
Proc. Natl. Acad. Sci. U.S.A. 78, 1446-1470, 1981				
A; Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinopeptides.				
A; Reference number: A73513; MJID:81199473; PMID:6262803				
A; Accession: A37513				
A; Molecule type: mRNA				
A; Residues: 44-68 <CHU>				
R; Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.				
PBS Lett. 232, 56-60, 1988				
A; Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to two fragments.				
A; Reference number: S02443; MJID:88211875; PMID:2966748				
A; Accession: S02443				
A; Molecule type: protein				
A; Residues: 373-374 <MBD>				
C; Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide A.				
C; Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha, beta, gamma).				
C; Superfamily: fibrinogen beta/gamma homology <FRG>				
F; 215-464; Domain: fibrinogen disulfide ring homology <FRG>				
F; 215-464; Domain: fibrinogen beta/gamma homology <FRG>				
F; 6/Binding site: pyrrolidine carboxylic acid (Gln).				
F; 6/Binding site: sulfate (Tyr) (covalent) #status experimental				
F; 211/Binding site: carbohydrate (Asn) (covalent) #status predicted				
F; 211/Binding site: carbohydrate (Asn) (covalent) #status experimental				
F; 371-373/Cleavage site: Arg-Thr (plasmin) #status experimental				
Query Match 19.8%; Score 470; DB 1; Length 468;				
Qy	9	LSSAVIATYGFIVVANNETEEIKDERAKVCPVRJESRGKCEEAEGCPYCVSLPPLTIGL	68	Qy 9 LSSAVIATYGFIVVANNETEEIKDERAKVCPVRJESRGKCEEAEGCPYCVSLPPLTIGL 68
Db	18	LSAACAA----YVATRNCCLIDERFSSYCP-----TGIADFUVNQTSV	60	Db 18 LSAACAA----YVATRNCCLIDERFSSYCP-----TGIADFUVNQTSV 60
Qy	69	PKQFSSRIEVPKVQNLIKEIVVNLKKSCQDCKLQADDNGDPGRNGLLIPSTGAPGEVDN	128	Qy 69 PKQFSSRIEVPKVQNLIKEIVVNLKKSCQDCKLQADDNGDPGRNGLLIPSTGAPGEVDN 128
Db	51	DKDLRTLEGILQYENKTEARELVKA----IQISYNPDQ-----	96	Db 51 DKDLRTLEGILQYENKTEARELVKA----IQISYNPDQ----- 96
Qy	229	RVRE-ESEYVNKLSELKNAKEEINVLHGLEKLNLYVNMANIENYVDISKV	177	Qy 229 RVRE-ESEYVNKLSELKNAKEEINVLHGLEKLNLYVNMANIENYVDISKV 177
Db	97	-PSKPMVNEASATKNSKSMEEI----MKYETLISTHESTIRFLQEYVNSNSQK	145	Db 97 -PSKPMVNEASATKNSKSMEEI----MKYETLISTHESTIRFLQEYVNSNSQK 145
Qy	178	ANLTFWNSLDGKCSKCPQECIQSRPVQHLYKDCSDYIAIGKRSSETTYT-PQPQRS	237	Qy 178 ANLTFWNSLDGKCSKCPQECIQSRPVQHLYKDCSDYIAIGKRSSETTYT-PQPQRS 237

Db 146 VNLDRKVQCLEANCQE-PCQDTVK---IHEVYGRICODVANKGAKESGLYFIRE-LKAKG 200
 Qy 238 FEVYCDMETMGGWTVLQARLQDGSTNFTRTWDYKAGFGNL-----RREFWLNDKHL 291
 Db 201 F-WVYCEIDLGSGNWTQFKRLDGLSLDFKRNLYQKEFGHLSPTGTGNTEFWLQNEK-HL 260
 Gy 292 LTKSKEM-LLRILEDENGFLYALYDQFVANEFLKVEHVGHV-NSTGDRL----- 343
 Db 261 ISTQQS-PVYVRLICLEDWNGTSITAYASERVYTGENDKTY-LTAYAFIGGGDAGDFGDF 320
 Qy 344 --R-FNKGH-NFDLKEFTPEKDNDYPSGNCGLYSSGMWEAULSNLKGH---- 395
 Db 321 GEDSSDKETFSNMGQFSTEDSDKRY-EGNCIAEVGIGWMNKSHAGHLNGVYQCGTY 379
 Qy 396 --QKVRGVNRNCFWGTWPGYSEAHPGYKS---SFKEAKMMIRP 434
 Db 380 SKTSPGYDNGLWATW-----KSRWIVSYKKTT-KLIIIP 413

RESULT .1
 PGHUB
 fibrinogen beta chain precursor [validated] - human
 N;Alternate names: coagulation factor ;
 N;Contains: fibrinopeptide B
 C;Species: Homo sapiens (man)
 C;Date: 24 Apr 1984 #sequence revision 31-Mar-1993 #text change 08-Dec-2003
 C;Accession: B41568; A90439; B90469; 137389; A94433; A9C437; A94309; G54223; AC0321; B371
 R;Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
 R;Chung, D.W.; Harris, J.E.; Davie, E.W.
 A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
 A;Reference number: A90439; MUID:9134474C; PMID:2102623
 A;Accession: B41568
 A;Molecule type: DNA
 A;Residues: P,193-491 <CH>
 A;Accession: B90469
 A;Molecule type: RNA
 A;Accession: B90469
 A;Cross-references: GB:J3C29; NID:9182429; PID:N-AAA52123-1; PTC:G18243C
 R;Huber, P.; Dalton, C.; Courtous, G.; Laurent, N.; Assouline, Z.; Marguerie, G.
 A;Title: Characterization of the 5' flanking region for the human fibrinogen beta gene.
 A;Reference number: 137389; MUID:87146453; PMID:3029722
 A;Accession: 137388
 A;Status: translated from GB/EML/DBJ
 A;Molecule type: DNA
 A;Residues: 1-38 <HUS>
 A;Cross-references: EMBL:X05018; PID:93140G; PID:CAA28674-1; PID:931401
 R;Henschen, A.; Lottspeich, F.; Sculthorpe, C.; Sjöström Petersson, E.
 in Probes of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, P.
 A;Title: Human fibrinogen sequence, sulfur bridges, glycosylation and some structural
 A;Reference number: A94433
 A;Contents: carbohydrate binding
 A;Accession: A94433
 A;Molecule type: protein
 A;Residues: 31-137; 'QS'140-144; 'QF'147-491 <HEN>
 R;Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
 Biochemistry '86, 68-76, 1979
 A;Title: Amino acid sequence of the beta chain of human fibrinogen.
 A;Reference number: A90437; MUID:79124640; PMID:422779
 A;Accession: A90437
 A;Molecule type: protein
 A;Residues: 31-144; 'QF'147-231; 'D'1233-330; 'E'332-491 <KAT>
 R;Blomback, B.; Hessel, B.; Hoggs, D.
 Thromb. Res. 8, 639-651, 1976
 A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.

A;Reference number: A94339; MUID:76225080; PMID:936108
 A;Contents: disulfide bonds
 A;Accession: A94039
 A;Molecule type: protein
 A;Residues: 31-112; 'B'1-4-137; 'QS'140-144; 'QF'147-148 <BL0>
 R;Kunitake, S.T.; Carlsson, C.T.; Sjöu, K.; Proctor, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A;Title: Identification of proteins associated with apolipoprotein A-I-containing lipo
 A;Reference number: A54223; MUID:94162201; PMID:817655
 A;Accession: GS4223
 A;Molecule type: protein
 A;Residues: 164-274 <KJN>
 A;Note: identification of tryptic peptides from high-density lipoproteins
 R;Henschen, A.; Lottspeich, F.; Xehl, M.; Southan, C.
 J.M. N. Y. Acad. Sci. 408, 28-43, 1993
 A;Title: Covalent structure of fibrinogen.
 A;Reference number: A90037; MUID:832544370; PMID:6575689
 A;Contents: annotation; review; disulfide bonds
 R;Gardlund, B.; Hessel, B.; Marguerie, G.; Blomback, B.
 Eur. J. Biochem. 77, 595-610, 1977
 A;Title: Primary structure of human fibrinogen. Characterization of disulfide-contains
 A;Reference number: A91249; MUID:77245993; PMID:895533
 A;Contents: annotation; disulfide bonds
 R;Doolittle, R.F.; Takagi, T.; Watt, K.; Boura III, H.; Cottrell, B.A.; Cassman, K.G.;
 in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Fo
 A;Title: The structures of fibrinogen and fibrin.
 A;Reference number: A94437
 A;Contents: annotation; disulfide bonds
 R;Doolittle, R.F.
 A;Title: Fibrinogen and fibrin.
 A;Reference number: A90041; MUID:84305751; PMID:6383194
 A;Contents: annotation; review; EM structure; polymerization; ligands
 R;Schung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
 Anz. N. Y. Acad. Sci. 408, 449-456, 1993
 A;Title: Cloning of fibrinogen genes and their cDNA.
 A;Reference number: A90328; MUID:83254384; PMID:6575700
 A;Contents: annotation
 R;Kirschbaum, N.E.; Budzynski, A.Z.
 J. Biol. Chem. 265, 13663-13676, 1990
 A;Title: A unique proteolytic fragment of human fibrinogen containing the Alpha CCN-
 A;Reference number: A37117; MUID:90137977; PMID:2143188
 A;Contents: annotation; hematin cleavage site
 A;Note: hematin, a protease from Haementia ghilianii, the giant South American leec
 C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which clea
 gulation sites responsible for the formation of the soft clot.
 C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabi
 ger), and between alpha chains (weaker) of different monomers.
 C;Comment: All fibrinogen chains are synthesized in the liver.
 A;Gene: GDB:FGB
 A;Cross-references: GDB:119130; OMIM:134930
 A;Map position: 4q28-4q28
 A;Introns: 38/3; 102/3; 16/1; 24/1; 278/1; 320/1; 415/2
 C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PTR:
 F1-30) domain; (or 4-10 or 15-30) signal sequence #status predicted <SIG>
 F131-491/2Product: fibrinogen beta chain; Glycoprotein; liver; Plasma; pyroglyutamic
 F131-491/2Product: fibrinopeptide B #status experimental <MAP>
 F145-491/2Product: fibrin beta chain #status experimental <APT>
 F145-47/Region: polymerization site
 F199-228/Domain: fibrinogen disulfide ring homology <FBG>
 F228-48/Domain: fibrinogen beta/gamma homology <FBG>
 F131/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status experiment
 F144-45/Cleavage site: Arg-Gly (thrombin) #status experimental
 F195/Disulfide bonds: interchain (to alpha-55) #status experimental
 F106/Disulfide bonds: interchain (to alpha-68) #status experimental

F;110/Disulfide bonds: interchain (to gamma-45); #status experimental F;223/Disulfide bonds: interchain (to alpha-184); #status experimental F;231-316,241-270,424-437/Disulfide bonds: #status experimental F;394/Binding site: carbohydride (Ash); #covariant	Query Match: Best Local Similarity 19.4%; Score 461; DB 1; Length 491; Matches 133; Conservative 57; Mismatches 161; Gaps 14;	Matches 130; Conservative 69; Mismatches 158; Indels 70; Gaps 17; Qy 20 SSAYLATGGELVANNETEETIDERAKDVCVRLESRGKCEAGECPYQSLPPLPTIQLP 69 Db 14 SLAIISSAFGNIPNTONCILDGRGEYCPT-----TCGJS 50
Qy 27 TEEIKDERAKCVCVRLESRGKCEAGE----CPYQSLPPLPTIQLP-QF-SRIEEVFK 80 Db 81 TQKVERVKAPEA-----GGTLHADPDGLVTCPTGCQLQEALIQQERTPIRNSTYDELIN 132	Qy 70 KQFSR1EE-VFKEVNQNLKEIVNSLKKSCQDCKLQADDNGDFGRNGLLPPTGAPSEVGDN 128 Matches 133; Conservative 57; Mismatches 161; Gaps 14;	Db 51 DFNRYQEVNVDPLQYLENLTQISNTSGT-----IEHLISGKPKATSPQA1-----DE 1C5
Qy 81 EVQSLKEITNS-----LKRSCOCJCLQADORGDPGRNGLLPESTGAPGVGDNRVREL 133 Db 133 NVEAVSQTSSSFOMYLKLQDJWQKROKVKON-----165	Qy 129 RVELESEVNKLUSSELKNAKE-EINVLHGRLEKLNLUVRNNNIENYVDSKANLTIVVNSL 187 Db 106 MTQSKSKTCWML-TDVKNNYQYEENLY-LQEVYSSNOKKI-FJLKOKANLEL-----156	Db 106 MTQSKSKTCWML-TDVKNNYQYEENLY-LQEVYSSNOKKI-FJLKOKANLEL-----156
Qy 134 ESEVNKLSSLKNAKEEINVLRH-EKLNLYMMNNIENYVDSKANLTIVVNSLDGKCSK 193 Db 166 ENVNEYSS-----LEKFLQLY-DETAVSNIPIPNLVRSLKSIQK 211	Qy 188 DGRQSKCPSQEQIQSRSRVOHQIYKDCSYAIGKRSSETYRTVTPDERSNEVYCDMETM 247 Db 157 -QCQQ-PORDTQ--IQEFQGKDCQEVANKGARLSGLIYIKELAKQQFLVTCIEPPS 210	Db 188 DGRQSKCPSQEQIQSRSRVOHQIYKDCSYAIGKRSSETYRTVTPDERSNEVYCDMETM 247 Db 157 -QCQQ-PORDTQ--IQEFQGKDCQEVANKGARLSGLIYIKELAKQQFLVTCIEPPS 210
Qy 194 CPSSEQIQ----SRPVQHQLYKQCSDDYYAIGKRSSETYRTVTPDERSSEFVYCD 243 Db 212 2ESDVAQNEYCRTPCTVSNCNPVPGSGBCE:RKGETSETKYLQPESSVKPVRYCO 271	Qy 248 GGGMVTLVQARLGSTNFTRTWDYKAGFG---NURREFWLGNDKHLLTJKSKEM--ILR 301 Db 211 GSATVIIQRLLGSVNHFRNRYQYREFGYJSPNDKTEFNGNEK-HLLSQSTIPIYVMR 270	Db 211 GSATVIIQRLLGSVNHFRNRYQYREFGYJSPNDKTEFNGNEK-HLLSQSTIPIYVMR 270
Qy 244 METHGCGKTYUQARLGSTNFTRTWDYKAGFG-----LBBRMUQGKTH 291 Db 272 MTFENGGRVQINQRQDGSDVFRKNDPQKGGSVQVATMDGNYCGLPGFYLGNDKRSC 332	Qy 302 IDELDENGVELYALYDCOFYVANEFLKYLHYGNY-NGTAZDAL-----RENHYH -NH 351 Db 271 TELEDWSQSKSTDAYSYSTERLGSEKDNTFRFTAYFIGDGAFAFDGDFDGPSPDFYTSH 330	Db 302 IDELDENGVELYALYDCOFYVANEFLKYLHYGNY-NGTAZDAL-----RENHYH -NH 351 Db 271 TELEDWSQSKSTDAYSYSTERLGSEKDNTFRFTAYFIGDGAFAFDGDFDGPSPDFYTSH 330
Qy 292 2TKSKEMKIRIDDEDFPGVELYALYDCQYWVANEFLKYLHYGNYTAGDAE.R-----344 Db 332 LTMGMPTEILLEMEDWKDKVKAHYGGTVQNEAKRQKISUNVKYRTAGNLMQDSCLN 391	Qy 352 ZLKEFETTDKNDRYPSCNGGYYSSGWWFACLSANLNGKYYH-----QKXRGVRN 403 Db 331 NGNGQFSTTDKNDKPF-DGNCASQDGSQWWXNRCHAHHNGKYYQGTTYSSEADSGSPSGYDN 389	Db 352 ZLKEFETTDKNDRYPSCNGGYYSSGWWFACLSANLNGKYYH-----QKXRGVRN 403 Db 331 NGNGQFSTTDKNDKPF-DGNCASQDGSQWWXNRCHAHHNGKYYQGTTYSSEADSGSPSGYDN 389
Qy 345 -FNGHYN-HDLKFETTPDQDNDRY----PSNNGLYSSGWWFDACLSANLNGKYY-----394 Db 392 GENBTMTHNGMFESTYRDNDGMLTSBPKQCSKEDGGHWWNRCHAMPNPGRYWGG 451	RESULT 13 JC598C Ficolin-A precursor - mouse C:Species: Mus musculus (house mouse) C:Accession: JC5980 C:Cross-references: DDBJ:AB007813; NID:92957011; PID:D1026054; PID:G2 C:Experiment: Liver C:Source: 06-May-1998 #sequence_revision: 29-May-1998 #text_change: 18-Feb-2000 C:Title: Ficolin-A precursor - mouse R:Fujimori, Y.; Harumiya, S.; Fukumoto, Y.; Miura, Y.; Yagasaki, K.; Tachikawa, H.; Fu Biomed. Biophys. Res. Commun., 244, 796-803, 1998 A:Title: Molecular cloning and characterization of mouse ficolin-A. A:Reference number: JC5980; M2D:9805801; PMID:9325745 A:Accession: JC5980 A:Molecule type: mRNA A:Residues: 1-334 <FU> A:Cross-references: DDBJ:AB007813; NID:92957011; PID:D1026054; PID:G2 A:Experiment: Liver C:Source: This protein consists of both collagen- and fibrinogen-like domains. C:Title: Ficolin beta/gamma homology E:1/21/Domain: signal sequence #status predicted <SIG> E:15/64-68/16/Domain: collagen-like #status predicted <COL> E:123-334/Domain: fibrinogen beta/gamma homology <FBG>	Query Match Score 19.0%; Best Local Similarity 34.4%; Pred. No. 6.5e-24; Matches 114; Conservative 35; Mismatches 106; Indels 76; Gaps 12;
Qy 395 --HQKYRGVRGFLRGTWPGSEAHRGGYKSSFEKAKMMP 434 Db 452 YTDMAXHG7TDGTVWWRKG-----SWY-SMRKMSMK-ZP 486	Qy 107 GDPRNGLLP--STGAPGEVGDNRVREJESEVNKLSELKNAKEEINVLRGRLKLNLY 164 Db 74 GSPQRMG--PAGSKGEPGTMSPPGYKGEKSDTGAAPS--LGEKELG-----115	Qy 107 GDPRNGLLP--STGAPGEVGDNRVREJESEVNKLSELKNAKEEINVLRGRLKLNLY 164 Db 74 GSPQRMG--PAGSKGEPGTMSPPGYKGEKSDTGAAPS--LGEKELG-----115
RESULT 12 A3167C fibrinogen gamma chain - African clawed frog C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1995 C:Accession: A32670; 151416 R:Pastor, R.L.; Moskowitz, J.E.; Smith Jr., L.H.; Schoenberg, D.R. Biochemistry 29, 2599-2605, 1990 A:Title: Estrogen regulation of Xenopus laevis fibrinogen gene expression. A:Reference number: A32670; MUID:90241882; PMID:2334684 A:Accession: A32670 A:Status: Preliminary A:Molecule type: mRNA A:Residues: 1-438 <PA> A:Cross-references: GB:J02894; NID:924139; PID:AAA49739; L: PID:92241440 R:Shattuck-Charyea, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J. McL Cell Endocrinol. 72, 213-220, 1990 A:Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenopus A:Reference number: 15-416; MUID:91146806; PMID:2289632 A:Accession: 151416 A:Molecule type: mRNA A:Residues: 1-58 <BA> A:Cross-references: GB:M35548; NID:9224144; PID:AAA03247; L: PID:92241442 R:Shattuck-Charyea, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J. Blood Coagulation Factor X 1, 173-183, 1990 A:Title: Blood coagulation C:Keywords: fibrinogen gamma chain; fibrinogen beta/gamma homology F:173-413/Domain: fibrinogen beta/gamma homology <FBG>	Qy 165 NMNNNENYVDSKVANLTFFVNNSLDGKCSKCPSPQEQIQSRRVQHLLIYKDCSDYYAIGKRSS 224 Db 116 -----DTLQRGRG-----RSQCDLRLTRG-FUT 137	
Query Match: Best Local Similarity 19.2%; Score 456; DB 2; Length 438; Best Local Similarity 30.4%; Pred. No. 5e-24;	Qy 226 ETYRV-TPQPKNSSEVYCDMETMGGWTWQARLDGSTNFTTMDYKAGFGNLRRFHN 283 Db 138 GWYTHILPDCR--PLVLCMDVGGWTWQRRVGSIOFRDSYKSGFGNLGTEFW 195	Qy 226 ETYRV-TPQPKNSSEVYCDMETMGGWTWQARLDGSTNFTTMDYKAGFGNLRRFHN 283 Db 138 GWYTHILPDCR--PLVLCMDVGGWTWQRRVGSIOFRDSYKSGFGNLGTEFW 195

RESULT 14

D44234 fibronectin alpha chain precursor, extended splice form - human
 N: Alternative names: coagulation factor I
 N: Contains: fibrinopeptide A
 C: Species: Homo sapiens (man)
 C: ID: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
 C: Accession: D44234; B44234
 C: Accession: D44234; B44234
 C: Accession: D44234; B44234
 C: Accession: D44234; B44234
 A: Status: transcribed from GB/EMBL/DBJ
 A: Molecule type: mRNA; DNA
 A: Residues: 1-866 <FJ2>
 A: Cross-references: GB:MS8569; NID:G182406; PID:G182407
 A: Note: neither the complete nucleic acid sequence nor the complete translation are shown
 A: Accession: B44234
 A: Molecule type: mRNA; DNA
 A: Residues: 605-866 <FJ2>
 C: Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
 C: Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleavage sites responsible for the formation of the scot clot.
 C: Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabilizer), and between alpha chains (weaker) of different monomers.
 C: Comment: All fibrinogen chains are synthesized in the liver.
 C: Genetics:
 A: Gene: GB:FGA
 A: Cross-references: GDB:119129; CMIM:134820
 A: Map position: 4q28.4-q28.5
 A: Map position: 18p3; 603; 122/1; 171/2
 A: Note: the list of introns is incomplete
 C: Complex: The fibrinogen molecule is a hexamer containing two sets of three non-identical domains in the core. Two three-chain coils emerge from this core and connect it to distal domain nodes.
 C: Function:
 A: Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into a fibrin clot.
 A: Pathway: blood coagulation
 C: Superfamily: human extended splice form fibrinogen alpha chain: fibrinogen beta/gamma
 C: Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
 F: 20-35/Product: fibrinopeptide A #status experimental <AP>
 F: 36-185/Domain: signal sequence #status predicted <SIG>
 F: 57-185/Domain: fibrinogen alpha chain, extended splice form #status predicted <FGA>
 F: 591-593/Region: cell; attachment: (R-G-D) motif
 F: 629-863/Domain: fibrinogen beta/gamma homology <FBG>
 F: 22-160/Banding site: phosphate (Ser) (covalent) #status: experimental
 F: 35-16/Cleavage site: Arg-Gly (thrombin) #status: experimental
 F: 55/55/Disulfide bonds: interchain (to alpha-47) #status: experimental
 F: 64/64/Disulfide bonds: interchain (to beta-95) #status: experimental
 F: 180/180/Disulfide bonds: interchain (to gamma-49) #status: experimental
 F: 184/184/Disulfide bonds: interchain (to beta-106) #status: experimental
 F: 288-419/Binding site: carbohydrate (Asn) (covalent) #status: absent
 F: 322/Cross-link: isopeptide (Lys) (interchain to Glc-2-P-asmin inhibitor) #status: absent
 F: 347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status: experimental

F: 461-491/Disulfide bonds: #status: experimental
 F: 527,558,575,591/Binding site: carbonyl (Asn) (covalent) #status: predicted
 F: 686,831/S:binding site: carbohydrate (Asn) (covalent) #status: predicted
 Query Match 19.0%; Score 451; DB 2; Length 866
 Best Local Similarity 32.5%; Pred. No. 2-8e-23;
 Matches 136; Conservative 51; Mismatches 137; Indels 94; Gaps 21;
 Cy 90 KEVONDEKIVNSLKLRSQCCDKLCLADDNG--DPGNGLLP 117
 E:3 476 KEV--TKEVWTS--EDGSDCP-EAMDGLTSGIGTLDGFHRHPDEAATPDATSTGKTFP 532
 Cy 116 S7GAP--GEVGDENRYRELESEVNKLUSSELMAKEEINVHLGRL-----KLN 162
 Db 521 GFFSPMVGEEF ---VETTERSGE-SGIVFNTKESSHHGIAAEFPGRGSSSSYSKOFTS 585
 Cy 163 LYMMNANIENYDVKSYKANLTIVVNS-LDJKCSKCPSEQC1QSREPGHJLYKDCSDY---YA 218
 Db 586 STSYNRGDSPESTEKSYSKADEAGSEADHEETHSTRGHAKSRPV----RDCCDDVLQTHP 640
 Cy 219 IGKRSSEPTYRTPDPKNSSEVYCOMETTMGGWTVLQARDLGINSFTWQDYRAGFGNL 278
 Db 641 SGTSQG-1NVIKLPGSSKITSVYCDGTSLGGMLLICORDGSLSNFNRTRDQYKRGRGSL 695
 Cy 279 ---RREFWLGNDKTHILTLTSEKMI.LRILEDENGVELAYDQCYVANEFLKIRLVN 334
 D:3 755 NDEGEFGLWDGYLHLITQ-RGSVVEREEDWAGNEY-HFRVGSSDEGHALQVSS 757
 Cy 335 YNGTAGDAL-----RFKPHYNEDNLKPFPTPDKDNDRYPGSGNCGLYSSGMNFDACU 385
 Db 758 YEGTAGDALIEGSVVEEGAAETSHNNMQ---FSTFADDOWE-NCAEYVGGHAYNNNC 813
 Cy 386 SANLNGKMY-----HKNYKGRGNGIWTGWTGVSSEAHPGGKSSPFKXAKMIRP 434
 Db 8-4 AAFLNLGTYPPGGSYDPRNNNSPVE-TENGVWVNSFRGAD-----YSLRAVRMIRP 862

RESULT 15

A15084 fibrinogen-related protein A precursor - sea cucumber (Parastichopus parvimensis);
 C:Species: Parastichopus parvimensis
 C:Accession: A35084
 R:Xu, X.; Doolittle, R.F.
 P:OC. Natl. Acad. Sci., U.S.A. 87, 2697-2101, 1990
 A:Title: Presence of a vertebrate fibrinogen-like sequence in an echinoderm.
 A:Reference number: A35084; PMID: 23192754; PMID: 23192755
 A:Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-282 <XTR>
 A: Cross-references: GB:M31326; NID:G161164; PID:G161165
 C:Superfamily: fibrinogen beta/gamma homology <FBG>
 F: 67-230/Domain: fibrinogen beta/gamma homology <FBG>
 Query Match 18.8%; Score 446; DB 2; Length 282;
 Best Local Similarity 43.2%; Pred. No. 1.3e-23; Gaps 9;
 Matches 93; Conservative 33; Mismatches 75; Indels 22; Gaps 9;
 Cy 2:1 KDCSDYY--AIGKR-SSEMYRVTDPDKNSSEPVYCDMETMGGMWTVLQARLGDSTNFTR 267
 Db 68 RDCYDILQSCSGSPGQQYTOPGSG-LIKVYCDMETDEGGWTVFQR RIDGTINFYRS 126
 Cy 266 WQDYKAGFGNLRREFNGNOKIHLTKSMELRIDLEDDNGVELYALYPOFYVANEFLK 327
 Db 127 WSYYQTGFGNLNTEFW-GNDNTHYLTSQGDYELRVE-LNPNHAYAKYKMFRI GDSFSE 186
 Cy 328 Y23HVGNYNTGDALEFREYNHDLKPFPTPDKDNDRYPGSGNCGLYSSS---WWFDAC 384
 Db 187 YLLVGLYSGTAGDSLAY----HNMTMRFSYTDNDVY-SINCASHSSYGRGAMYWYKSC 240
 Cy 395 LSANLNQKYYHQKYRGNGIWFWGTPGVSEAHPGGYKSSFKEAKDMIR 433

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Page 10

D2 241 LLNLNGQYY-DYSGAPS-TYMSYLPGNDQIP-----FAEMKLNRK 280

Search completed: November 5, 2003, 16:48:13
Jcb time : 28.0749 secs

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CM protein - protein search, using sw model

Run on: November 5, 2003, 15:59:02 ; Search time 19.3292 Seconds
(without alignments)
1067.536 Million Cell updates/sec

Title: US-09-9C2-563-2

Perfect score: 2378
Sequence: 1 MKAANWWLSSAVLATYGFLL...GYKSSFFKEAKMIRPKHFKP 433

Scoring table: BLASTMY62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 5

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41. *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8 Result No. Score Query Length DB ID Description

No.	Score	Query	Length	DB	ID	Description
1	2378	10C.0	433	FGI2_HUMAN	Q15485	FCN2_HUMAN
2	1853	77.9	432	FGI2_MOUSE	PC260	rattus norvegicus
3	525	22.1	496	AGI2_MOUSE	075616	homo sapiens
4	524	22.1	375	AGI2_BOVIN	P55033	homo sapiens
5	523	22.0	495	AGI2_PIG	P22105	homo sapiens
6	522	22.0	495	AGI2_HUMAN	Q9Y5C1	homo sapiens
7	511	21.5	463	FIBB_CHICK	P24831	homo sapiens
8	506.5	21.3	312	FIBI_HUMAN	Q29116	mus musculus
9	486.5	20.5	498	AGPI_HUMAN	P00632	gallus gallus
10	481.5	20.4	493	ANL2_MOUSE	Q9Y096	homo sapiens
11	481.5	20.3	453	FIBG_HUMAN	P10099	gallus gallus
12	463.5	20.3	498	AGPI_MOUSE	Q9Y182	mus musculus
13	480.5	20.2	493	ANL2_HUMAN	Q9Z1P3	mus musculus
14	479	20.2	477	FIBB_PETRA	P10477	parastacoides
15	473	19.9	497	AGPI_RAT	P02675	rattus norvegicus
16	471	19.8	468	FIBB_BOVIN	P02676	bos taurus
17	473.5	19.8	503	AGPI_MOUSE	P92WHE	mus musculus
18	467	19.6	491	A321_BOVIN	P12920	bos taurus
19	462	19.4	444	FIBG_BOVIN	P12793	bos taurus
20	461	19.4	491	FIBB_HUMAN	P12675	homo sapiens
21	456	19.2	418	FIBG_XENLA	P17634	xenopus laevis
22	451.5	19.1	479	FIBB_RAT	P14480	rattus norvegicus
23	452	19.0	334	FCN1_MOUSE	Q7O165	mus musculus
24	451	19.0	491	FIBA_HUMAN	P02671	homo sapiens
25	450	18.9	503	AGP4_HUMAN	Q9Y264	homo sapiens
26	446	18.8	262	FIBA_PARPA	P19477	parastacoides
27	441	18.5	782	FIBA_RAT	P06399	rattus norvegicus
28	438	18.4	335	FCN1_RAT	Q9wts8	rattus norvegicus
29	428.5	18.0	432	FIBG_PETNA	P04115	petromyzon
30	428	18.0	339	FCN2_RAT	P27556	rattus norvegicus
31	427.5	18.0	741	FIBA_CHICK	P14448	gallus gallus
32	427	18.0	326	ANL2_HUMAN	P00632	homo sapiens
33	421.5	17.7	306	FCN2_MOUSE	Q7O497	mus musculus

ALIGNMENTS

RESULT 1						
FGI2_HUMAN	ID	FGI2_HUMAN		STANDARD;	PRT;	439 AA.
AC	Q14314;					
DT	16-CCT-2001 (Rel. 40, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DT	15-SEP-2003 (Rel. 42, Last annotation update)					
DE	Fibroleukin precursor (Fibrinogen-like protein 2)	(pT49).				
GN						
GS	Homo sapiens (Human);					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
NCBI_TAXID=606;						
OX						
RN						
RP	SEQUENCE FROM N.A.					
RC	TISSUE-Small intestine;					
RC	Medline=95369700; PubMed=7642206;					
RR	Ruegg C.; Pytela R.;					
RT	"Sequence of human transcript expressed in T-lymphocytes and encoding a fibrinogen-like protein.";					
RT	Gene 160:257-262(1995).;					
RT	Gene 160:257-262(1995).;					
RT	SEQUENCE FROM N.A.					
RA	Yuwaraj S.; Liu X.; Marsden P.; Levy G.					
RT	Cloning and characterization of Hg12; the human counterpart to the mouse gene Fg12.;					
RT	Submitted (NOV-1998) to the EMBL/GenBank/DDJB databases.					
RA	SEQUENCE FROM N.A., AND VARIANT: GIC_53.					
RA	Rieder M.J.; Arnett T.Z.; Carrington D.P.; Chung M.-W.; Lee K.-L.; Poe, C.L.; Ozuna M.; Yi Q.; Nickerson D.A.; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.					
PL						
PL						
RF	SEQUENCE FROM N.A.					
RC	TISSUE-Blood;					
RC	Medline=1238257; PubMed=12477932;					
RA	Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.; Koide S.; Carninci P.; Casavant T.L.; Schuster T.B.; Schueler G.D., Sherman C.M., Schaefer C.F., Bhattacharya S., Hsieh F., Klaasen R.D., Coillins F.S., Wagner L., Shemer R., Altschul S.F., Zeiberger B., Buetow K.E., Prange C., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.-J., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Carlson P.H., Bonaldo M.F., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Abramson R.D., Mullahy S.J., Bozak S.A., McEvany P.C., McKernan K.J., Malek Z.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W., Villalba D.K., Muzyz D.M., Sodergran E.J., Lu X., Gibbs R.A., Pahey C., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko A.Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield S.R.N., Krzywinski M.-E., Skalska U., Smilus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).					

[5]	CHARACTERIZATION MEDLINE=98309432; PubMed=9547227; Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M., Argraves S., von Fliegener V., Pytelka R., Rueegg C.; "Characterization of human fibroblasts, a fibrinogen-like protein secreted by T lymphocytes.", J Immunol. 161:138-147(1998).
-!-	FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT MUCOSAL SITES.
-!-	SUBUNIT: HOMOTETRAMER: DISULFIDE-LINKED.
-!-	SUBCELLULAR LOCATION: Secreted.
-!-	TISSUE SPECIFICITY: CONSTITUTUTIVE EXPRESSED IN CYTOTOXIC T-CELLS.
-!-	SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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	EMBL: 236531; CABAB5298.1; . EMBL: AF104045; ADD1C85.1; . EMBL: AF104C4; ADD1C85.1; JOINED. EMBL: AF68959; ADD1C85.1; . EMBL: 36033830; AH33820.1; . P-R: 137391; 137391. HSSP: P02671; IF2D. Genew: HGNC:3696; PGJ-2. NM: 603251; . GO: GO:0005976; C: extracellular; TAS. GO: GO:00005974; C: fibrinogen beta chain; TAS. InterPro: IPR022181; Fibrinogen_C. SMART: SMC0186; FBG_1. PROSITE: PSC0514; FIBRIN_AGC_DCM1N; 1. T-cell; Glycoprotein; Signal; Polymorphism. SIGNALLING; SIGNAL; 23 CHAIN; 24 DOMAIN; 210 DISULFID; 213 DISULFID; 242 DISULFID; 371 CARBOHYD; 25 CARBOHYD; 25 CARBOHYD; 179 CARBOHYD; 235 CARBOHYD; 263 CARBOHYD; 336 VARIANT; 53 SEQUENCE; 419 AA; 50228 MW: 6756788E466 CRC64;

	Query Match Best Local Similarity 100.0%; Score 2378; DB 1; Length 439; Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 MKLANWYISSLAVATYGLFLVANNEETEIKDERAKDVCVPRJESRGKCREAGECPYQVS 60 2 LPPPLIQPKPSRKEEVPEKVNQKKEEINVLRGRLEKLNLYNNNTENYVDVKVNL 180 1 MKLANWYISSLAVATYGLFLVANNEETEIKDERAKDVCVPRJESRGKCREAGECPYQVS 60 61 LPPPLIQPKPSRKEEVPEKVNQKKEEINVLRGRLEKLNLYNNNTENYVDVKVNL 120 61 LPPPLIQPKPSRKEEVPEKVNQKKEEINVLRGRLEKLNLYNNNTENYVDVKVNL 120 121 APGEYGDNRVRELESENKLSSELKNAKEEEINVLRGRLEKLNLYNNNTENYVDVKVNL 180 122 APGEYGDNRVRELESENKLSSELKNAKEEEINVLRGRLEKLNLYNNNTENYVDVKVNL 180 123 TEVNSLDGKSKCPSQEQIQRPHQJLIVKDCSYYAIGKPSSETYRTPDKKSSFEV 240

RJ	Radziejewski C., Compton D.L., McClaire J., Aldrich T.H., Papadopoulos N., Daly T.C., Davis S., Saco T.N., Yancopoulos G.D.; RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo angiogenesis"; Science 277:55-60(1997)
CC	-.- FUNCTION: BINDS TO TIE2 RECEPTOR AND COINTEGRATES BLOOD VESSEL MATURENATION STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY BE CONTEXT DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE ANGIOGENIC SIGNAL.
CC	-- SPECIFICULAR LOCATION: Secreted
CC	-- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR REMODELING.
CC	-- SIMILARITY: Contains 1 Fibrogen C-terminal domain.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation on the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch) or send an email to license@isb-sib.ch.
CC	EMBL: AF004326; AAB62189; 1; - .
DR	HSSP: P02671; 1FDZ.
DR	WGD: MGII:1202890; Aspt2.
DR	InterPro: IPR000181; Fibrinogen_C.
DR	Pfam: PF00147; fibrinogen_C; 1.
SMART: SMCO186; FBG; 1.	
PROSITE: PS000514; FIBRIN_ANC_DOMAIN; 1;	
KW	Angiogenesis; Glycoprotein; Coiled coil; signal.
FT	SIGNAL 1 18.
FT	CHAIN 1 496.
FT	DOMAIN 159 256 (POTENTIAL).
FT	DOMAIN 280 496 COILED COIL (POTENTIAL).
FT	DISEASED 284 313 FIBRINOGEN C-TERMINAL.
FT	DISULFID 437 450 BY SIMILARITY.
FT	CARBONYD 89 89 BY SIMILARITY.
FT	CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 56616 MW: FA3021FE401C410 CRC64; SEQUENCE 496 AA: - .
Query Match	22.1%; Score 525; DB 1; Length 496;
Best Loca:	Similarity 32.9%; Pred. No. 3e-28;
Matches 127;	Conservative 65; Mismatches 154; Indels 40; Gaps 9;
Qy	61 LPPPLTPOLPKQFSRIZEEVFKEYVQLNLKIVNSLKKSCDKCKQADDNGDFGRNCQLLPSTG 120
Db	142 LTDVEAQVNQTRL---EQQLQHS:STNKLEQIQLDTSEINLNQNRSFL-----191;
Qy	121 APGEVGDNVRLEEVNKLSEVNAKEEINVHLGRL-----EKLNLYMNNTENY 172
Db	192 7DSKVNLTFVNSLQDGCKSCPKPSQEQISQPSRVQHLYKDCSDYYAGKRSESTYRVPD 232
Qy	244 LCKQQHDLMERTNMSLUTMMSSPNSSKSSAIIKEQQTFRDCAEIFSGLTTSGYIUTFP 303
Db	233 PKNSFFEVYCDMETMGGWTVLQARDLGSTNFRTWDYKAGFGNLRFREPLGNDKHL 292
Qy	304 NSTEEFKAYCDMVGGGWTIQHREDSVDFQRTWKEYKEBFGNPDIQEYTGNEFVSQL 363
Db	293 TKSKEMLRILEDFTGVEVYALDQFYVANEFLKYLHVNYNGTAGDALRFNMHYNHD 352
Qy	364 TGQHRYVVKQLKDMEGNEAHSLSYDFLAGEESNRIHLTGTGTAKISSISOPGSDD- 422
Db	353 LKPFPTPDKNDKDRYPSSGNGLYSSGWFDACLSANLNGKYHQKRGVR-NGLFWGTWPF 411

423	--FSTKDSNDKCIC-KCSQNM-SGGWWFDACGPNSLNQYYPQKNTNKFNGIKWVYNNK	478
412	GVSEAHPGGYKSSFEAKMMP-RPKHP	437
479	G-----SGY--SKATMM-RPADF	496
RESULT 4		
GP2_BOVIN		
AGP2_BOVIN	STANDARD;	PRT;
C77802; G9TSK0; C41		375 AA.
16-OCT-2001 (Rel. 40, Created)		
16-OCT-2001 (Rel. 40, Last sequence update)		
28-FEB-2003 (Rel. 41, Last annotation update)		
ANGIOPoietin-2 (ANG-2); (Fragment).		
ANGPT2; CR ANG2.		
Bos tauris (Bovine); Eukarya; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.		
NCBI TaxID=9913;		
_		
SEQUENCE FROM N.A.		
SEQUENCE OF 219-355 FROM N.A.		
TISSUE=Adrenal cortex;		
MEDLINE=99054148; PubMed=9840613;		
Medline ID=8451664; PubMed=9776732;		
Mandriota S.J.; Pepper V.S.; Goede V.; Schmitz T.; Kämänen S.; Koziar D.; Augustin H.G.; "Analysis of blood vessel maturation processes during cyclic ovarian angiogenesis"; Circ. Res. 83:852-859 (1998).		
-!- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL MATURATION STABILITY MEDIED BY ANGIOPOETIN-1. ITS FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH AS VEGF, ANG-2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE ANGIOGENIC SIGNAL.		
-!- SUBCELLULAR LOCATION: Secreted.		
-!- CYCLE: CYCREDRESSED THROUGH LUTEOLYSIS. THIS COULD REFLECT THE REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN THE MIDSTAGE CORPUS LUTEUM.		
-!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.		

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EMBL; AF094699; AAC62490; 1; -;		
EMBL; AF029294; AAC78285; 1; -;		
HSSPDB; P02671; 1FZD.		
InterPro; IPR002181; Fibrinogen_C.		
Pfam; PF00147; fibrinogen_C.		
SMART; SM001186; FBG; 1.		
PROSITE; PS00514; FIBRINAG_C_DOMAIN; 1.		
Anglogenesis; Glycoprotein_C_domain; Coiled coil.		
NON_TER	1	COILED COIL (POTENTIAL).
DOMAIN	10	138
DOMAIN	159	375
DISTILIFID	159	192
		RY SIMILARITY

DISULFID	316	329	BY SIMILARITY.
PT	13	13	N-LINKED (GLCNAC. . .)
CARBOHYD	31	31	N-LINKED (GLCNAC. . .)
PT	120	120	N-LINKED (GLCNAC. . .)
CARBOHYD	183	183	(POTENTIAL). . .
PT	272	S -> L (IN REF. 2).	(POTENTIAL). . .
CONFICT	375	AA;	6F096C4A5C8C050A CRC64;
SQ	SEQUENCE		
Query Match	22.1%	Score 524.5;	DB 1; Length 375;
Best Local Similarity	34.2%	Pred. No. 2, 3e-28;	Gaps 14;
Matches 216; Conservative	58;	Mismatches 139;	Indels 65;
OY	61	LPPTIQPKQFSRVEEVKEYEQLKEIV-NSLKKSCD-	-CKLQADDNGDPGRN 1:3
Db	22	LTPVEAQTLNQTRL- ---ELQQLBHSLSNKLEQI	DTSKQ-----DKNS 69
OY	114	LLLPSTGAPGEVGDNRVPELSEEVNKLSELSEKNAEINVHGR	-----LEK-UNLVN 165
Db	70	FL-----EKVLDMEKHIVQLRSIKEEQLQVLVSQNSNIELEKQLVAT	118
OY	166	MRI-----ENTVDSKVANLTQFVNSLQGKCSKCPQEQTOSRPVCHLIVRDCSDYIAIG	220
Db	119	VRSVSLQKQHDLMETVNQNLTLMSNPSYSSLLADEQI	-----IFRCGAFAKSG 170
OY	221	KRSSETYVTPDKNSSFEVYCDMETMGGMWTVQARLGSTNFRTTWQDYKAGFGNLR	R 280
Db	171	LTTSGVYLTFPNSTEE-KAYCDMTEGGMMWTVIQREDDGVDFQRTWKEYKVGFGNPSG	230
OY	28:	EPLNLGNDKIHLLTKSKEYN:LRDLEDENGVELYALDQFYVANEFLKYRLHVGVNYNTAG	340
Db	23:	EHLIGNEFTVSQUTGGRYVILKHLRDWGNBASYLDFYLVSNEELNRYTHLKGLTGTA	G 250
OY	34:	DAFRENKYNHD-KFETTPEKDNDRYPGSNCGLYYSSGAWFDACLSANLNQSKYHQYRG	400
Db	29:	KISSISQGND---FSTKDAENDKCLIC-KCSQM:DGGMWEDACGPNSNLQYYQRONT	345
OY	40:	VR-NGIFGTW2PSVSEAHPGGYKSFFXEAQKMIRZGHF	437
Db	346	NKFNGIKYWWG-----SGY--SLRATTMIRPADE	F 375
RESULT 5			
AGP2_PIG	ID	AGP2_PIG	STANDARD;
AC	C9BY7;	PRT;	496 AA.
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Acipicopetin-2 Precursor (ANG-2).		
GN	ANGPT2.		
OS	Sus scrofa (Pig)		
CC	Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Garteriodactyla; Suisna; Suidae; Sus.		
CX	NCBI_TaxID:98223;		
RN	[1]		
RP	SEQUENCE FROM N_A.		
RX	MEDLINE:21153163; PubMed:11230987;		
RA	Kim I., Moon S.O., Han C.Y., Park Y.K., Moon S.K., Kim J.J., Koh G.Y.:		
RT	"The angiopoietin-tie2 system in coronary artery endothelium prevents oxidized low-density lipoprotein-induced apoptosis."		
RT	Cardiovasc. Res. 49:812-881 (2001).		
CC	-!- FUNCTION: Binds to Tie2 receptor and counteracts blood vessel maturation/stability mediated by angiopoietin-1. Its function may be context-dependent. In the absence of angiogenic inducers, such as VEGF, Ang-2-mediated loosening of cell-matrix contacts may induce endothelial cell apoptosis with consequent vascular regression. In concert with VEGF, it may facilitate endothelial cell migration and proliferation, thus serving as a permissive angiogenic signal (by similarity).		
CC	-!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.		
CC	-!- SWISS-PROT entry is Connexin. It is produced through a collaborative		

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CC EMBL; AP33228; AAC:4993.1; .
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C; 1..
 DR SMART; SM0085; FBG; 1..
 DR PROSITE; PS00514; FIBRIN AG-C DOMAIN; 1..
 CC Argogenesis; Glycoprotein; Coiled coil; Signal.
 SEQ ID N: 1
 FT SIGNAL 1 : B
 FT CHAIN 19 : B
 FT ANGIOPOTIN-2.
 FT COILED COIL ((POENTIAL).
 FT DOMAIN 130 :
 FT FIBRINGER C-TERMINAL.
 FT DISULFID 280 :
 FT DISULFID 284 : 313 BY SIMILARITY.
 FT DISULFID 437 : 45C BY SIMILARITY.
 FT CARBOHYD 89 : 9 N-LINKED GLCNAC. (POTENTIAL).
 FT CARBOHYD 119 : 9 N-LINKED GLCNAC. (POTENTIAL).
 FT CARBOHYD 133 : 133 N-LINKED GLCNAC. (POTENTIAL).
 FT CARBOHYD 151 : 151 N-LINKED GLCNAC. (POTENTIAL).
 FT CARBOHYD 240 : 240 N-LINKED GLCNAC. (POTENTIAL).
 FT CARBOHYD 304 : 304 N-LINKED GLCNAC. (POTENTIAL).
 SQ SEQUENCE 496 AA; 56911 NW; 33802BE224FEE59C CRC64;
 Query Match 22.0% Score 523; DB 1; Length 496;
 Best Local Similarity 34.9%; Prid. No. 4; i=28;
 Matches 121; Conservative 49; Mismatches 120; Indels 57; Gaps 8;
 Gaps 120;
 Qy 127 DNPVRELESEVKLSS-
 Db 171 EKQIUDOTSINKLQDKNSPLEKVKVLDMEKHIVCLOSKEEDQLOVLSKNSIIEL 230
 Qy 169 TEINYDSKRYAN-
 Db 231 EKQVLTAVNNSLVQKHDLMETVHNLTMSNSAHSVYAKEQI-----IFR 282
 Qy 212 DCSDYYAIGKRSETYRVTPDPKNSFSEVYCDMSTMGGSWTVQARLGSTNTFRTRQDY 271
 Db 283 DCAAZAFKSGUTTSGNTLTPNSTETRAYCDMTEGGGWTVVORREGSVDQRTNEY 342
 Qy 272 KAGCAGLRLREFWLGDKNUHILTKSKEMILPIDEENGELYALYQSYVIANEFKRYH 331
 Db 343 RMGFSPSGHWHNLGEFVSCTYNOVRYKIHDRWEGNEAYXIEHYLSSBFNRH 4C2
 Qy 332 VGNYNNGTAGDALRERKSYHNDLKEFTTPXCDNDRYPSGNGLYJYSSGHNEDACLSAHLNG 391
 Db 403 LKGITGTGAKTISIOPGND---FSTKADNCICIC-KCSQVLTGGRNFDAQPSNNG 457
 Qy 392 KYHQHQYGVY-NGFWGTWPGVSEAHPG3YKKSREAKMMIRKFHF 437
 Db 458 MYVQRQNTNKENG1KWyWKG-----SSY-SLKATMMIRFADP 495
 RESULT 6
 AGP_2_HUMAN STANDARD FRT; 496 AA.
 AC ID AGP2_HUMAN; Q9NRR7; C992Y7;
 DT 16-OCT-2001 (Rel. 40, Created);
 DT 16-OCT-2001 (Rel. 40, Last sequence update);
 DE Angiopoietin-2 precursor (ANG-2).
 GN ANGP2.
 CS Homo sapiens (HUMAN); Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TAXID=9606;
 RN [1] SEQUENCE FRCM N.A. (ISOFORM 1).
 RC TISSUE=Lung;

MEDLINE=97349327; PubMed=9204896;
 Maisonneuve P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J., Radziejewski C., Compton D., McClaire J., Aldrich T.H., Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.; "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo angiogenesis"; Science 277:55-60(1997).
 [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RX SEQUENCE=99126459; PubMed=9922494;
 RA Tanaka S., Mori M., Sakamoto Y., Makuchi M., Sugimachi K., Wards J.P.; "Bio-logic significance of angiopoietin-2 expression in human hepatocellular carcinoma"; J. Clin. Invest. 103:341-345(1999).
 RN 3.
 RF SEQUENCE FRCM N.A. (ISOFORM 2).
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=2003C9815; PubMed=1076762;
 RA Kim J., Kim J.-H., Ryu Y.S., Jung S.H., Nah G.J., Nah G.Y.; "Characterization and expression of a novel alternatively spliced human angiopoietin-2"; J. Biol. Chem. 275:18552-18556 (2000).
 RL FUNCTION: BINDS TO TIE RECEPTORS AND COUNTERACTS BLOOD VESSEL MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY BE CONTEXT-DEPENDENT IN THE ABSENCE OF ANGIOGENIC INDUCERS SUCH AS VEGF. ANG-2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE ANGIOGENIC SIGNAL.
 CC SUBCELLULAR LOCATION: Secreted.
 CC ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=1;
 CC Sequence=VSP 001540;
 CC IsoID=O15123-1; Sequence=Displayed;
 CC Name=2;
 CC IsoID=O15123-2; Sequence=VSP 001540;
 CC Name=3;
 CC IsoID=O15123-1; Sequence=Display;
 CC SIMILARITY: Contains 1 fibroningen C-terminal domain.
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 CC EMBL; AF04327; AAC83190; .
 CC EMBL; ABC09865; BAA559C; .
 CC HSSP; P02671; LFZD.
 CC NM: 601922; .
 DR GO: GO:0003615: C: extracellular space; TAS.
 DR GO: GO:0003102; P: receptor binding activity; TAS.
 DR GO: GO:0034511; P: cell growth and/or maintenance; TAS.
 DR GO: GO:007165; P: signal transduction; TAS.
 DR Interpro; IPR02184; Fibroin_C_C.
 DR SMART; SMWC186; FBG; 1.
 DR PROSITE; PSC0514; FIBRIN AG-C DOMAIN; 1.
 DR KW Angiogenesis; Glycoprotein; Coiled coil; signal; Alternative splicing; POTENTIAL.
 DR SIGNAL 1 : 16 ANGIOPOIETIN-2.
 DR FT DOMAIN 17 : 496 COILED COIL (POTENTIAL).
 DR FT DOMAIN 130 : 256 FIBRINOGEN C-TERMINAL.
 DR FT DISCUFLID 280 : 496 BY SIMILARITY.
 DR FT DISCUFLID 284 : 313 BY SIMILARITY.
 DR FT DISCUFLID 437 : 450 BY SIMILARITY.
 DR FT SIGNAL 1 : 16 ANGIOPOIETIN-2.
 DR FT DOMAIN 17 : 496 COILED COIL (POTENTIAL).
 DR FT DOMAIN 280 : 496 N-LINKED (GLCNAC); (POTENTIAL).
 DR FT CARBOHYD 89 : 89 N-LINKED (GLCNAC); (POTENTIAL).
 DR FT CARBOHYD 119 : 119 N-LINKED (GLCNAC); (POTENTIAL).
 DR FT CARBOHYD 133 : 133 N-LINKED (GLCNAC); (POTENTIAL).
 DR FT CARBOHYD 151 : 151 N-LINKED (GLCNAC); (POTENTIAL).

FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 97 148 Missing (in Isoform 2).
 FT /FTID-VSP 0C1540
 FT CONFLICT 268 268 MISSING (IN REF. 2).
 SQ SEQUENCE 496 AA; 56919 XW; 562A58847A7385C CRC64;
 Query Match 22.0%; Score 522; DB 1; Length: 496;
 Best Loca: Similarity 27.9%; Pred. No. 4 Se-8;
 Matches 138; Conservative 74; MisMatches 159; Indels 124; Gaps 15;

Qy 43 LESRGKKE--EAGECPYQVSPLPL--TIO-LPKQFSRIEEVFKENQN 84
 Db 26 MDSIGKQXQVQHGSCTYTFIPEMDNCRSSSSPVNSAVQRDALEYDDSVQRQLQLEN 85
 Qy 85 LRE-----IVNSLRSKCCQCKLQADDGDPGRNGLLPSGTTGAEVDN--- 128
 Db 86 INENNTOWMLKLENYQDNMKKXENVIQONQVN----QTAVMIEGTNLNQ 134
 Qy 129 -----RVRELSEV-----NKLSSELKNAKEFINTVHLGR---LEKL 161
 Db 135 TAEQTRKLTDVAQVLNQQTTRIDLOLHS:STNRCEKQDCTSE:NKLQDQNSFLEEK 194
 Qy 162 NAV-----V-----NMNNTENYVDSKVANLT-----V 183
 Db 195 VLAMEDKHIZQLCSTEKEKDQQLQVJYSKNSKZIEELKKVATVNNSY:QKQQHQHLMET 254
 Qy 184 VNSLOGKSKCSKPCSQEQTSRQVPHLYKOCSDYYAIGKRSSETTVTPDANSRREVCD 243
 Db 255 VNLNLTMMSTSNSAKPQTVAKEQISFRQDCEVFSGHTINGVTLTPNSTEETKAYCD 314
 Qy 244 METMGGGWTIVLQDARLQSTNFRTWDYKAGFGLNREFNGNDKIH-LTKSKEMIJRD 303
 Db 315 MEAGGGGWTIVLQDARLQSTNFRTWDYKAGFGLNREFNGNDKIH-LTKSKEMIJRD 374
 Qy 304 LEQFGNGVELYA-YDQFYVANEFKYLRYEVNGNNGTAGDALRFKYNHDLKFETTPDKEN 363
 Db 375 LRDWGEAATSYLTERFLSSEETNRIHLKGDTGAKISSISQFQND---FS-KOGEN 430
 Qy 364 DRYPSGNMGJYSSGMWFDACLSANLNKGKYHCKYRGVR-NGIFGNTNPVSUEAHPGGYK 422
 Db 431 DKCIC-KCSONT-TGGWWFACOPSNLNGMYPQRONTNKENGKIRWYWKG---SGYI- 432
 Qy 423 SFFKEAKMMIRPFHF 437
 Db 483 -SLKATTMMIRPFHF 496

RESULT 7
 FIBB-CHICK STANDARD; PRT: 463 AA.
 AC CGC2020;
 DT 01-JUL-1993 (Rel. 26 Created;
 DT 15-SEP-2003 (Rel. 42 Last annotation update)
 DE Fibrinopeptide [Contains: Fibrinopeptide B]
 DE (Fragment).
 GN FIBB.
 OS Galus galus (Chicken).
 OC Bucaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianinae;
 Galus.
 OCBI -TaxID:9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
 RX MEDLINE=91182745; PubMed=200926;
 RA Weissbach L.; Cadoux C.; Procyk R.; Grierer G.;
 RT "The beta chain of chicken fibrinogen contains an atypical thrombin cleavage site.";
 RL Biochemistry 30:329C-3294 (1991). DOUBLE FUNCTION: YIELDING MONOMERS THAT POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.
 CC

CC SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC MISCELLANEOUS: CONVERSION OF FIBRINogen TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RECOGNISABLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLUT BY FACTOR XIIIA WHICH CATALYZES THE ESSILON (GAMMA-Glutamyl)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT MONOMERS.
 CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC
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 CC
 CC EMBL: M58514; AXA8770_1; .
 DR PIR: A38463; A38463.
 DR 1E13; 10-MAY-00.
 DR InterPro: IPR02181; Fibrinogen_C_1.
 PRIM: PF00147; Fibrinogen_C_1.
 SMART: SM00186; FBG_1.
 PROSITE: PS00514; FIBRIN_AS_C_DOMAIN_1.
 KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation; 3D-structure.
 CC
 CC NC TER : 1
 FT PEPTIDE : 17
 FT CHAIN : 18
 FT PRO RES : 5
 FT PEST : 5
 FT SSTE : 17
 DR FIBRINOPEPTIDE B.
 DR FIBRIN (BY THROMBIN, RELEASE CLEAVAGE (BY THROMBIN, RELEASE FIBRINOPEPTIDE B)).
 DR INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
 DR INTERCHAIN (WITH ALFA) (BY SIMILARITY);
 DR INTERCHAIN (WITH GAMMA) (BY SIMILARITY);
 DR INTERCHAIN (WITH ALFA) (BY SIMILARITY);
 DR DISULFID 69 69
 FT DISULFID 80 80
 DR DISULFID 84 84
 FT DISULFID 197 197
 DR DISULFID 201 201
 FT DISULFID 205 289
 DR DISULFID 215 244
 FT DISULFID 397 410
 DR CARBOHYD 367 367
 SC SEQUENCE 463 AA; 52678 MW; 2044CD49B79EC73 CRC64;
 DR
 CY Query Match: 21.5%; DB 1; Length: 463;
 CY Best Loca: Similarity 30.4%; Pred. No. 2-2e-27;
 CY Matches 137; Conservative 71; Mismatches 154; Indels 89; Gaps 16;
 CY 31 KDERAKDQCVPRVLESRGKC---EEAGE-CPYQVSLSLPPLT-QLPKQPSRLPPT-BEVFKEVQN- 64
 DR 51: QDQKAMKKGPIYIPDAGGCRPELDEGVZCPTGCE--LQTLLKQETKTPVLRDKDR 107
 CY 85 -----LKEIVNLSLKSCQDKLQADDNGDPGRNGLILPSTCPGEVGDNVRELE 134
 DR 108 VAKFSDITSMQVNNIDKLVKTKQKQRD----NDITLSENTMEMEHYNTK--D 159
 CY 115 SEVKNKLSEELQAAKEINVHLGRLEKLNLMVANNIENYVDSKVKANLTIVVNSLDGKCSKC 194
 DR 160 NLNNNIPSPSLRVRAVIDSLHKKQL-----ENAIATQT-----DYCRSPC 201
 CY 195 PSOEQIQSPRPVQHLYKQDSYIAIGKRSSETYRVT?DPKNSFEVYVCDMETXGGSWTIL 254
 DR 202 ---VASCNIPVSPGRCEDIVRKGGGETSEMYYIOPDPFTPYRYCDMETDNGWTLI 256
 DR 255 QARLDGSTNTFTWODYKAGFGNLRR-----EFLWGNDKKHLTKSKEMIILRID 303
 DR 257 QNQDGSNFNGRAWDEYKGRGIANIAKSGGKRYCDTGEYNGNQDKSSQLTKGPVKLVE 316
 CY 304 LEDFNGVELYALYDQFYVANEELKYLHVGNYNTAGDALR- FNKHYN- ---HDLX 354
 DR 317 MEDWNGDKVSALEYGGFTHNESENKYQOLSVSNYKQMEASOLYGGENRTYTHNGM 376

Query Match						
	Best Local Similarity	Score	Length	DB	DB ID	Length
Qy	31.1	506.5	312;			
Do	36.8*	543	219;			
Qy	13.1	186	119;			
Do	18	REI-SALEDCAGEQNRLAQVRLLETRVKQQVQKIQKOLLOENEVQLDKGDENTYIDLG-	75			
Qy	-6.7	LDGKCSKCPSEQIQSPRQVHILYKCSDDYYAIGKRSSETYRVTDPKNSSEFYQYQDMET-	246			
Do	76	-----SKRQ-----YACSELENDGYMLSGFYKIKLQSPAEFSYCDMSD	116			
Qy	24.7	MGGWTVLQARDGSTINFTRIWQDYKAGFQNL--REFWFLGNDKTHLLTKSKENYLRID	303			
Db	22.7	-GGWTVLQERDGSBNENRGKDYINGE3FVQKHGEYNNIGKRNHFLTQDYLKID	175			
Qy	30.4	LEDNGVELAYLYDQFYVANEFLKYLHVGNYNGTAGDAFLRFNKH-----YNHDLKFFT	357			
Db	17.6	LADPFRNSRYAYKPNFKVGDEKFNFLINIGEYSGTAGDSLGNFHFEQWMASHORMKFS	235			
Qy	35.8	TSDKDNDYPGNCNGLYSSGMWFDACLSANLNGKYVHQKYRG-VRNGIFWGTWPQUSER	416			
Db	23.6	TWDRDHENY-ENCAEBDOSGMWENCHSARLNQVYSSGPYTAKT-TNGIVWTW-----	288			
Qy	41.1	HPGYYKSFFKEAKMIRPKHFKP	419			
Db	28.9	-HGMWPSLKSUTWKRPNDFP	309			
RESULT 9						
AGP1_HUMAN	STANDARD:	PRT:	498 AA.			
ID: AC151765;						
AC: AC151765;						
DT: 16-OCT-2001 (Rel. 40, Created)						
DT: 16-OCT-2001 (Rel. 40, Last sequence update)						
DT: 28-FEB-2003 (Rel. 41, Last annotation update)						
DE: Atp1ioprotein-1 precursor (ANG-1).						
GN: ANGPT1 OR KIAA0033.						
OS: Homo sapiens (Human).						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo; Homo; NCBI Taxid=9606;

OX RN [1] SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.

RC TISSUE=Peritoneal lung; PubMed=8980223;

RX MEDLINE=97134663; PubMed=8980223;

RA DAVIS S., ALDRICH P.H., JONES P.F., Acheson A., Compton D.L., Jain V., RYAN T.E., BRUNO J., RADIEJEWSKI C., MAISONPIERRE P.C., YANCOPOLIOS G.D.;

RA "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by secretion-trap expression cloning.";

RT Cell 87:1161-1169(1996).

RN [2] SEQUENCE FROM N.A.

RP MEDLINE=12166954; PubMed=12166954;

RA NAKAJIMA D., OKAZAKI N., YAMAKAWA H., KIKUCHI R., OHARA C., NAGASE T.;

RT "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";

RT CURATION OF 330 KIAA cDNA clones.";

RL DNA Res. 9:99-106(2002).

RN [3] SEQUENCE OF 307-498 FROM N.A.

RP TISSUE=Bone marrow; MEDLINE=36051387; PubMed=7584026;

RC Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y., Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;

RT "Prediction of the coding sequences of unidentified human genes. V: analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1";

RT Cell 77:17-35(1994).

RN [4] SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.

RA NAKATSUKA M., KORAI K., SHIOZAWA S.;

RT "Human angiopoietin mRNA variant form.";

RJ Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

RP SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.

RA SHAN Z.X., YU X.Y., LIN Q.Y., FU Y.H., TAN H.H., ZHENG M., LIN S.G.; RT "Human angiopoietin-1 mRNA variant forms";

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

CC --!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS TYROSINE PHOSPHORYLATION, IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE ENDOTHELIAL AND SURROUNDING MATRIX AND MESANGIAL, MEDiates ECDC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE HEART EARLY DEVELOPMENT.

CC --!- PTM: GLYCOSYLATED.

CC --!- MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE IT CAN BE USED FOR SPECIFICALLY TARGETING TUNICA VASCULATURE OR FOR PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN ISCHEMIC HEART.

CC --!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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CC EMBL: U3508; AAB5057.1; -.

DR EMBL: BAB0273; BAB91325.1; -_INIT.

DR EMBL: AB084454; BAB91325.1; -.

DR EMBL: AY25504; AAM81745.1; -.

DR EMBL: AY243380; AAM92271.1; -.

DR ISSN: P02621; LFZD.

DR Genew: HGNC:494; ANGPT1.

DR NMIM: 601667; -.

CO GO:GO:005102; F:receptor binding activity; TAS.

CO GO:GO:0007165; P:signal transduction; TAS.

DR InterPro: IPR002181; Fibrinogen_C.1.

PFam: PF01474; Fibrinogen_C.1.

SMART: SMCC186; FBG; 1.

DR PROSITE: PS00514; FIBRIN_AC DOMAIN; Coiled coil; Signal; Polymorphism.

KW Angiogenesis; Glycoprotein; Coiled coil; Signal; Polymorphism.

SIGNAL 1 15

FT CHAIN 16 498

FT DOMAIN 81 119

FT DOMAIN 153 261

FT DOMAIN 284 498

FT DISULFID 286 315

FT DISULFID 439 452

FT CARBOHYD 92 92

FT CARBOHYD 122 122

FT CARBOHYD 154 154

FT CARBOHYD 243 243

FT CARBOHYD 295 295

FT VARIANT 269 269

FT /FTID=VAR 009940;

FT EXON SLIP PAGE.

SEQ SEQUENCE 498 AA; 57513 MW; SD5FA63AEFB6E920 CRC64;

Query Match 20.5%; Score 486.5; DB 1; Length 498;

Best Local Similarity 32.3%; Pred. No. 1.2e-25;

Matches 131; Conservative 59; Mismatches 136; Indels 79; Gaps 16;

Qy 61 LPFLTIQPKQSRI --- EYKVEVQNLKEIVNLSKSCQDKLQADDNGDPGRN 112

Db 145 LDTYETQVLNQS-SRLEIQLENS-LSTYKLEQLOOTNEIYIKE---- KN 19:

Qy 113 GLLPSIGAPGEVGENDNVRLESEVNKLSELUKNAAEIVVHLG-----RLBK-L 161

Db 192 SLL-----EHILEME---GKKEELDTKKEKENLQLGYTRQTYYIQLBEKQL 237

Qy 162 NLYNMANNENYVDVKAVNLTYVNNLSDGKCSK---CPSCBEGIOSRPFVQHIIYKQCSDY 217

Db 238 NRATTNN-SVLIQKQOLEMDTMVNLNVLTCTKVGLJKGGKREEKPL---FRDADVY 290

Qy 218 AIGKSSETYRV---TRDPKPSSEFEVYCYETMGSGWTQARIQDGSTMTRTWDYKA 273

Db 231 QAGFNKSGIIYTYYINNMPEPK---KVFCMYDVNGGWTIQHREGSLFCRGWKEYKM 346

Qy 274 GFGRNRREFLGNDKTHLTTKSKMLRID-LEDFGVNLAYLQDFVYVANEFLKYLHNG 333

Db 347 GFNPSEGVLGNEFIFATNTSQRQMPATYIENDWGNRAYSQYDRTGHQNQYBLYK 406

Qy 334 NYNTAGDAFLRKENHYNHDLKFTTPDKNDNDRYPGNCGJYSSGWFADCLUSANNGKY 393

Db 407 GHGTGAGQSSLILH-GAD---PSTRDACNDNCMC-KCALM-TGGWWFDACOPSNLNGMF 461

Qy 394 YHQ-KYEVYRNGI-FWGTAPEGVSEAHPGGKYSSEKFAEMMIREPKHF 437

Db 462 YTACQNHHEKLNG-KWHYFKGPS-----YSLRSTMMIRSPDF 496

RESULT 10

AND MOUSE STANDARD; PRT; 493 AA.

ID AN2_MOUSE ID: Q9R045;

AC 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).

GN AKPTL2 OR ARP.

CS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Craniata; Vertebrata; Eute-eostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murus.

CX NCBI TaxID:20090;

RN [1] SEQUENCE FROM N.A.

RP TISSUE=Heart;

RC MEDLINE=9943103; PubMed=10473614;

RA Kim J., Moor S.-O., Koh K.-N., Kim H., Uhm C.-S., Kwak H.-J., Kim N.-G.,

Koh G.Y.;
 "Molecular cloning, expression, and characterization of angiopoietin-related protein, angiopoietin-related protein induces endothelial cell sprouting";
J. Bio. Chem., 274: 26523-26528(1999);

- |- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN AUTOCRINE AND PARACRINE ACTION (BY SIMILARITY).
- |- SUBCELLULAR LOCATION: Secreted (By similarity).
- |- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMIS AND TESTIS.
- |- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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- R: SEQUENCE OF 75-286 FROM N.A.
C TISSUE:LIVER;
I MEDLINE=9219334; PubMed=1685103;
S "Zanelli T., Malcovati M., Tenchini M.;
Marchetti S., Zanelli T., Malcovati M., Tenchini M.;
DNA Seg. 1:149-142(1993).";
T [18] SEQUENCE OF 285-437 FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
R MEDLINE=85010379; PubMed=6092346;
P Forname A.J. Jr., Cummings D.E., Comau C.M., Kant J.A.,
C Craib G.R.;
T "Structure of the human gamma-fibrinogen gene. Alternative tRNA splicing near the 3' end of the gene produces gamma A and gamma B forms of gamma-fibrinogen.";
R [19] SEQUENCE OF 2C9-270 FROM N.A.
R MEDLINE=84069377; PubMed=6689367;
R Imam A.Y.A., Eaton M.A.W., Williamson R., Humphries S.;
T "Isolation and characterization of cDNA clones for the A alpha- and gamma-chains of human fibrinogen.";
R Nucleic Acids Res. 11:7427-7434(1983).";
T [10] SEQUENCE OF 411-453 (ISOFORM GAMMA-B).
R MEDLINE=8208993; PubMed=7006501;
R "Wolfenstein-Tode C., McFesson M.W.;
R "Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant (gamma-).";
R Biochemistry 20:6146-6149(1981).";
T [11] DISULFIDE BONDS.
R Doolittle R.F., Takagi T., Watt K.W.X., Bouma H., III, Correll B.A.,
R Cassman K.G., Goldbaum D.M., Dogiatti L.R., Friezner S.J.;
R Hirschson A., Lotspeich F., Kehl M., Southan C.;
R "The structures of fibrinogen and fibrin.";
R (In) Magnusson S., Ottessen N., Folmann B., Danø K.,
R Neurath H. (eds.);
R Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
R Pergamon Press, New York (1978).";
T [12] DISULFIDE BONDS.
R MEDLINE=7622508C; PubMed=936108;
R Blomback B., Hessel B., Hogg D.,
R "Disulfide bridges in NH2-terminal part of human fibrinogen.";
R Thromb. Res. 8:633-652(1973).";
T [13] QUATERNARY STRUCTURE, AND DISULFIDE BONDS.
R MEDLINE=83231465; PubMed=6830649;
R Hoeprich P.-J., Docitelle R. F.;
R "Dimeric half-molecules of human fibrinogen are joined through disulfide bonds in an antiparallel orientation.";
R Biochemistry 22:2049-2055(1983).";
T [15] SULFDATION.
R MEDLINE=9136996C; PubMed=1892942;
R Farrel D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.;
R "Recombinant human fibrinogen and sulfation of the gamma chain.";
R Biochemistry 30:9414-9420(1991).";
T [16] POLYMERIZATION SITE.
R MEDLINE=8430751; PubMed=6333194;
R Docitelle R. F.;
R "Fibrinogen and fibrin.";
R Annu. Rev. Biochem. 53:195-229(1984).";
T [17] POLYMERIZATION SITE.
R MEDLINE=85014892; PubMed=6592597;
R Hwang R.H., Varad A., Scheraga H.A.,
R "Lysine residues in the C-terminal region of fibrin polymerize to form a dimeric structure.";
R Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).";
R: Localization of a fibrin gamma-chain polymerization site within segment Thr-374 to Glu-396 of human fibrinogen.";
C R: segment Thr-374 to Glu-396 of human fibrinogen.";
I R: Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).";
S [18] POLYMERIZATION SITE.
R MEDLINE=81142375; PubMed=6451630;
R: Localization of a fibrin polymerization site.";
R: Olexa S.A., Budynski A.Z.,
R: RA J. Bioi. Chem. 256:3544-3549(1981).";
T [19] PLATELET AGGREGATION SITE.
R MEDLINE=84103545; PubMed=326808;
R Xicczak M., Timmons S., Lukas T.J., Hawiger J.;
R "Platelet receptor recognition site on human fibrinogen. Synthesis and structure-function relationship of peptides corresponding to the carboxy-terminal segment of the gamma chain.";
R Biochemistry 23:1767-1774(1984).";
T [20] PLATELET AGGREGATION SITE.
R MEDLINE=84103545; PubMed=326808;
R Plow E. F., Stouli A.H., Meyer D., Marguerie G., Ginsberg M.H.;
R "Evidence that three adhesive proteins interact with a common recognition site on activated platelets.";
R J. Bioi. Chem. 259:5388-5391(1984).";
T [21] CALCIUM-BINDING SITE.
R MEDLINE=85221382; PubMed=3160702;
R Plow E. F., Belli W.R.;
R Dang C.V., Ebert R.F.;
R: RA "Localization of a fibrinogen calcium binding site between gamma-subunit positions 311 and 336 by terbium fluorescence.";
R: RL J. Bioi. Chem. 260:9713-9719(1985).";
T [22] CALCIUM-BINDING SITE.
R MEDLINE=81054908; PubMed=9335457;
R: RA "Human plasma fibrinogen heterogeneity: evidence for an extended carboxy-terminal sequence in a normal gamma chain variant (Gamma-).";
R: RL Proc. Natl. Acad. Sci. U.S.A. 77:5069-5073(1980).";
T [23] CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
R MEDLINE=97169449; PubMed=9016719;
R X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
R: RX Yee V.C., Pratt K.P., Cote H.C.F., Le Trong I., Chung D.W.,
R: RA "Crystal structure of 30 kDa C-terminal fragment from the gamma chain of human fibrinogen.";
R: PT Structure 5:125-138(1997).";
T [24] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
R MEDLINE=97352277; PubMed=207064;
R: RA Pratt K.P., Cote H.C.F., Chung D.W., Sterkamp F.E., Davie E.W.;
R: RT "The primary fibrin polymerization pocket: three-dimensional structure of a 30-kDa C-terminal gamma chain fragment complexed with the peptide Gly-Pro-Gly-Pro.";
R: PT Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).";
T [25] Query Match 20.4%; Score 484.5; DB 1; Length 453;
Best Local Similarity 29.7%; Pred. No. 1..4e-25;
Matches 141; Conservative 56; Mismatches 178; Indels 99; Gaps 8
Q Y W-SVAVLATYGFLWVANNETEIKKDERAKDVSPLVRLESRGKCEAECPYVSLSPPTIQ
D D 19 FLSSTCVAA---YVATRDNCILDERFGSCTP-----TCGIADFSLTYQT
Q Y 68 LPKQFSR1EEVFKEVONLKETVNSLKSQCDOKLQADDNGDFGRNGLLPSGTGAEVGVD
D D 62 VDKDLSQSEJD1HGVENTSKEVQLKAIQ-LTKNPPESSXPNM1-----DAAT
Q Y 128 NRVELEEVNLSSLEKNAKEEINVLHGRLEKLNLYMNNTENYYDSKVANLTFTVNSL
D D 110 LISKRMKJEEIMKMYEASLTHDSSIRVY---EYZNNN----QKVNKLKEKVAOL

SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=2338257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.Y., Schuler G.D.,
RA Altshuler M.J., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEvany P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.C., Hulyk S.W.,
RA Villalba D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Farby J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwade J., Schmitz J., Myers R.Y.,
RA Butterfield Y.S.N., Krzywinski M.Z., Skalska U., Smailius D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analyses of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
CC AUTOCRINE AND PARACRINE ACTION.
CC -- SUBCELLULAR LOCATION: Secreted.
CC -- TISSUE SPECIFICITY: Widely expressed in heart, small intestine,
CC spleen and stomach. Also found in lower levels in colon, ovary,
CC adrenal gland, skeletal muscle and in prostate.
CC -- PTM: N GLYCOSYLATED.
CC -- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC This SWISS-PROT entry is copytight. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: AF125175; AAJ053157.1; -.
DR EMBL: BC012368; AAH12368.1; -.
DR HSSP: P02672; 1FZD.
DR GenBank: HGNC490; ANGGT1.2.
DR NM_000001; -.
DR GO: GO:000615; C: extracellular space; TIS.
DR GO: GO:000102; receptor binding activity; TAS.
DR GO: GO:000275; P: development; TAS.
DR InterPro: IPR002181; Fibrinogen_C.
DR SMART: PF00147; Fibrinogen_C.
DR SMART: SM0086; FBG.
DR PROSITE: PS000514; FIBRIN AG C DOMAIN, 1.
DR Signal: 1 22 POTENTIAL AGIOPETIN-RELATED PROTEIN 2.
FT CHAIN: 23 493 COILED COIL (PCVENTIAL).
FT DOMAIN: 76 155 COILED COIL (PCVENTIAL).
FT DOMAIN: 152 236 FBRINGEN C-TERMINAL.
FT DOMAIN: 438 456 BY SIMILARITY.
FT DISULFID: 278 443 BY SIMILARITY.
FT CARBOHYD: 430 164 N-LINKED (GUNAC. .) (POTENTIAL).
FT CARBOHYD: 192 192 N-LINKED (GUNAC. .) (POTENTIAL).
SQ SEQUENCE: 493 AA; 57104 MW; CF2ADCE53D185CA CRC64;
Query Match 20.2%; Score 480.5; DB 1; Length 493;
Best Local Similarity 30.9%; Pred. No. 3e-25;
Matches 117; Conservative 62; Mismatches 128; Indels 73; Gaps 12;

Qy 66 IQLPKFSRIEYFKEV---ON-KEIVNLSKRSQDKCKQADDNGDPGRNGLLPSTGA 121
Db 170 LQASLKYDLEKHYQHILATLAMNOSEIIAQLEFHCPV-----PSARPVPQPZPAA 220
Qy 122 PGEGVD---NRYRELESEVNKLSELSEKNAKEBINVLGRLEKLNVNMMNENYDSKY 177

DC 221 PRVYQPTTYR1-----INCISTNBIGSDONJKVLPPIPPMPIL----- 261
Qy 178 ANLTIVVNSLDGCKSKCPSEQIQTSRPFVQHLYKDCSDDYAYAKRSSETTYRTPDKRS 237
DB 262 -----TS-PSSTDKPSGP----WRCDCQALEGDHDTSIYLKPENTNL 302
Qy 238 FEYCDMETMGGMWTLQARLGDSTNTRDYKAGFGNLREFWGNDKHHLJTKSKE 297
DB 303 MQYACDQRDHDPGMWTVQRLGSVSNPFRNNTYKQGFGNDGEYMLGLENLYWLTNQGN 362
Qy 298 MIDDLDEFDNGVYELVYDQFWVANBPLKFLHVGVNNGTAGDALFRNHYNHDLKPF 357
DB 363 YKLVTMWDWSRKVKVEAYAASPLPESEYYKLREGYHGNAGDSTPW----HNKGQET 417
Qy 358 TPDKDNDRYPSGNCGLYYSGHWFDACLSANLNGKYY--HOKYRGYRNZFWGTWPGVS 414
DB 418 TLDRDHDVY-TGCAHYNQGGWYNNACAHSLNGWVFRGHYRSR-YQDGVIWAERFGC- 473
Qy 415 EAHPGGYKXSPKEAKMNP 434
DB 474 ----GSY-SLKRVMMP 487

RESULT 14
FIBB_PETMA STANDARD, PRT, 477 AA.
ID FIBB_PETMA STANDARD,
AC P02678;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibrinopeptide beta chain (Contains: Fibrinopeptide B) (Fragments).
CS Petromyzon marinus (Sea lamprey)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
CC Petromyzontiformes; Petromyzontidae; Petromyzontida; Petromyzon.
NCBI TaxID=7757;
RN [1];
RP SEQUENCE CF 1-36.
RX YEOLINE<7706679; PubMed=993898;
RA Cottrell B.A., Doolittle R.P.;
RT "Amino acid sequences of lamprey fibrinopeptides A and B and
RT characterizations of the junctions split by lamprey and mammalian
RT thrombins.";
RL Biochim. Biophys. Acta 453:426-438(1976).
PQ SEQUENCE OF 37-477. FROM N.A.
RX MED-NE-870582; Published=3190537;
RA Beuton V.L., Doolittle R.F., Pontes M., Strong D.D.;
RT "Complementary DNA sequence of lamprey fibrinogen beta chain.";
CC -- FUNCTION: FIBRINONE HAS A DCUB-E FUNCTION: Yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -- SUBUNIT: Hexamer containing 2 sets of 3 non-identical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -- MISCELLANEOUS: conversion of fibrinogen to fibrin is triggered by
CC thrombin, which cleaves fibrinopeptides A and B from alpha & beta
CC chains, and thus exposes the N-terminal polymerization sites
CC responsible for the formation of the soft clot. The soft clot is
CC converted into the hard clot by factor XIIIa which catalyzes the
CC epsilon-(gamma-glutamyl)lysine cross-linking between gamma chains
CC (stronger) and between alpha chains (weaker) of different
CC monomers.
CC -- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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or send an email to license@isb-sib.ch).

Query Match		Score 479.5; DB: 1; Length: 477;	
Best Local Matches		Pred. No. 3-4e-25;	
131: Conservative		Mismatches 138; Indels 113; Gaps 15;	
Qy	DISULFID	29 EKDERAKDVCPPRLESRGKCEBAGECYQVSLPPTQLPKQFSRRIEVFKEVQNKEI	204
Cb	DISULFID	100 EJREELIKQRDPR-----YKISMK-----QNLTYF 126	
Qy	DISULFID	89 VNSLKKSCQQCCKQADDONGDEGRNGLLPLSTGAPGEVGDNRVRELRESEVNKLSSSELZRAK	148
Cb	DISULFID	127 INSFDR -----MASSDNNTKON-----VQTLRRRLNSSSSTHYNAC 162	
Qy	SEQUENCE	149 EENIVLHQRLEKLNLYNNNNZENYVDSKVAVLTFVUNISLDGKCSK-----CPSEQEQIQSRP	204
Cb	SEQUENCE	163 KEI---ENRYKEYKI----RIESTVAGSLRSNKSVLLEHRLAQRMEMEAITQKOKELCSAP 215	
Qy	DISULFID	265 -----VOLHYYKDCSDYYAIGRKSSSETYRVTPDKNSFRYCDMMBTMGGSWTVLQARL	256
Cb	DISULFID	216 CTVNCRPVVPSGMHCEDIYRNGRTSEAYIOPDLFSEPPKRYCDMSHGGKWTYQNRV 275	
Qy	DISULFID	259 DGSTNFTRTWDQYKAGFGNLR-----REFWLGNDKTHLLTTSKEMILRID-EDF 307	307
Cb	DISULFID	276 DGSNFARDWNTYKAFFNTIAFGNGKSCICNIPEYWLGLTVHQHLFQHTQCVLFDSNDW 335	
Qy	DISULFID	308 NGVELYALYDQFVYVANEEFLKYRLHVGYNYNGTAGDAL-----RFYKHYN_HCLKEFT	358
Cb	DISULFID	336 EGSSVYACYASERPFNEAQGYRLWEDYSGNAGNALLLEGATCNGN2RMTMHGQFST 395	
Qy	DISULFID	359 PDKDNEYR-----PSGNCLYYLSSGGWWFACLSANLSSYY-----HQKRYGVRSNCFW 407	407
Cb	DISULFID	396 FORDNDNNPGDETCKSREDAGGWVNRCHAANENGRRYNGGTYTQEADYGTDDSVNW 455	
Qy	DISULFID	408 GTWPGVSEAHPGGYXKSFSFEAKCMYIRPK 435	435
Cb	DISULFID	456 MNWKG-----SMY-SVROMAMKLIRPK 475	

Cy	114	LJLUPSTGAPGEVGNCVRLESEYKLSSELKNAKEEINVLHGEJLKUN:VANNINNIENTV	173
Db	193	LJ...-.-.-.-. EH KILEMEGK -	222
Qy	174	ESKVALFVNNSLOGCKSKCPSEQCIQR-----PVQHLI-----	29
Db	223	- - UTRQFIIQEJEQSLRATSNNSVLQKQBLIMCTVHNLSLCTREVLKGKREEE	279
Qy	210	- - YKD CSDYYAIGKRSSETYRV - - TPDPKNSSEFVY COMETMGSGNTVLCARLDGSTN	263
Db	280	KPFRD CADYQAFNSKGTYIVFNXPBK - - KVFCMDVNEGGWVIQHREDDGSJD	335
Qy	264	FRTWDQDKAGFNLNRREFWLGDKHILTKSKEMI:RILEDCEFGVLYALYDFYVAN	323
Db	336	FORGWEEFKMFGSPRSPEGYWLGNFIFIATQSQRGMYR ELMDCENRAYSCPRFHIGN	395
Qy	324	EFLKYRLHVGNYNGTAGDAIRFNKYNHDLKFPTDKENDRYPSGNCGLYYSSSSWWFDA	383
Db	396	QKONYRLVKGHTSTAGROSSLILH-GAD - - FTKDAANDNCMC - KCALMLTGCKWWFDA	450
Qy	384	CISANLNGSKYIHO KYRGYRGINGWTGPGVSEAHPGYKSSPKFNEAKMRIPGF	437
Db	451	CGPSNNDNMFTYAGONHGGLNGKWHYFGPS-----YSRSTSTMKAIRPDE	497

Search completed: November 5, 2003, 16:46:19
Job time : 20 3392 secs

Qy	181 TPIVNSLDGKCS-SKCPSEQIQLQSRPVQHLLYKDCSDYYA;GKRSETETYVTDFRNSSTE 239	Db	293 YSSGMWFDACLSANLNGKYNNQRYGVNRGIFWGTPGVSCAHPGKPFPRCAKMRP 352
Db	183 TPIVNSLDGKCS-SKCPSEQIQLQSRPVQHLLYKDCSEYYT;GKRSETETYVTDFRNSSTE 242	Qy	435 XSFKP 439
Qy	240 VCDMETHMGGMWTVLARLDGSTNFRTRWCDYKAGFNLREFWLGNDK;HLLTSKSEMI 299	Db	353 XSFKP 357
Db	243 VCDMETHGGGMWTVLARLDGSTNFRTRWCDYKAGFNLREFWLGNDKHLLTSKSEMI 302		
	RESULT 3		
Qy	300 LRIDLDFNGVLYALYDQFYVANEFLKYRLHVNINGTAGDA;RNFKHNHDLKFETTP 359	QBWNE4	PRELIMINARY;
Db	303 LRIDLDFNGFLKYLASDHFYVANEFLKYRLHVNINGTAGDA;RNFKHNHDLKFETTP 362	ID OBWNE4	PRT; 148 AA.
Qy	360 DKNDORYPSGNGMGLYSSGMWDACLSANLNGKYTHOKRGVRNGIFWGTPGSEAHPG 419	AC OBWNE4;	Created)
Db	363 DRDNDRYPSGNGMGLYSSGMWDACLSANLNGKYNNQRYGVNRGIFWGTPGSEAFQFG 422	DT 01-MAR-2002 (TREMBLrel. 20; Last sequence update)	
Qy	420 GYKSSFEAKNMIRPKHFKP 439	DT 01-OCT-2002 (TREMBLrel. 22; Last annotation update)	
Db	423 GYRSSFEAKNMIRPKYFKP 442	DE Similar to fibrinogen-like 2.	
Qy	424 GYKSSFEAKNMIRPKHFKP 439	OS Homo sapiens (Human).	
Db	425 GYRSSFEAKNMIRPKYFKP 442	OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
	NCBI_TaxID=9606;	OX NCBI_TaxID=9606;	
	[1]	RN [1]	
	RP SEQUENCE FROM N.A.	RC TISSUE/LUNG;	
	RA Strausberg R.; Submitted (DB-2001) to the EMBL/GenBank/DDBJ databases.	RA Strausberg R.; Submitted (DB-2001) to the EMBL/GenBank/DDBJ databases.	
	RL EMBL: BC017813; AAC: 7813.1; MW: 45687DBA37CC7F21 CRC64;	DR EMBL: BC017813; AAC: 7813.1; MW: 45687DBA37CC7F21 CRC64;	
	SQ SEQUENCE	SEQUENCE	
Qy	1 YKLANYWLLSSAVIATYGFIVANNTEEFIKDERAKDVCPVRLSERGKCEAGECPYCUS 60	Query Match 31.5%; Score 750; DB 4;	
Db	1 YKLANYWLLSSAVIATYGFIVANNTEEFIKDERAKDVCPVRLSERGKCEAGECPYCUS 60	Best Local Similarity 99.3%; Pred No. 7.1e-43; Length 148;	
Qy	2 LPLPTICLPKQSRRIEVKEVQNLEKIVNLSKKSCQCKLQADDNGDPERNLGLPESTG 120	Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Db	2 LPLPTICLPKQSRRIEVKEVQNLEKIVNLSKKSCQCKLQADDNGDPERNLGLPESTG 120	Qy 31.5%; Score 750; DB 4;	
Qy	3 AFGEVGDNRVRELESEVNKLSELK 145	Best Local Similarity 99.3%; Pred No. 7.1e-43; Length 148;	
Db	3 AFGEVGDNRVRELESEVNKLSELK 145	Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
	NCBI_TaxID=116;	RC STRAIN=Sprague-Dawley;	
	RN [1]	RA Richlik D.P.; Chien E.; Philippe M.;	
	RP SEQUENCE FROM N.A.	RA "FGL2 Expression in the Sprague-Dawley Rat";	
	RR "FGL2 Expression in the Sprague-Dawley Rat";	RT "FGL2 Expression in the Sprague-Dawley Rat";	
	RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
	DR FSSP: P02671; IPI2D;	DR SMART: SM00186; FBG: 1	
	DR InterPro: IPR0211; Fibrinogen_C; _;	DR PROSITE: PS00514; FIBRIN_AGC_DOMAIN; 1	
	DR SMART: SM00186; FBG: 1	DR PROSITE: PS00514; FIBRIN_AGC_DOMAIN; 1	
	DR SEQUENCE: P00514; FIBRIN_AGC_DOMAIN; 1	DR SEQUENCE: P00514; FIBRIN_AGC_DOMAIN; 1	
	SQ SEQUENCE 357 AA; MW: 40966 MW; 31183D9402EBB9 CRC64;	QNDQ1 PRELIMINARY;	
Qy	75 TEVFKEVKONLKEVNSLKKSCQDKLQADNGDPERNLGLPESTGAFGVGVNVRVLE 134	AC QNDQ1; PRELIMINARY;	
Db	1 VEVLVEKRVTLCEAVSLSLKKSCQDKLQADNGDPERNLGLPESTGAFGVGVNVRVLE 134	DT 01-OCT-2000 (TREMBLrel. 15; Created); DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)	
Qy	135 SEVNKLSELKNAKEEINVLRQJERKLNLYNANNENYDVKVANLTFVNSLDGKCSKC 134	DT 01-DEC-2001 (TREMBLrel. 19; Last annotation update)	
Db	53 S0VNKLSELKNAKEEINVLRQJERKLNLYNANNENYDVKVANLTFVNSLDGKCSKC 134	DE Fibrinogen-like protein.	
Qy	195 PSQECIORSRPHOLIYKDCSYYAIGKRSSETTYTDFPNSSEVYCOMETGAGNTLV 254	DN Ciona intestinalis;	
Db	113 PSQECIORSRPHOLIYKDCSYYAIGKRSSETTYTDFPNSSEVYCOMETGAGNTLV 254	OS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogena;	
Qy	113 PSQECIORSRPHOLIYKDCSYYAIGKRSSETTYTDFPNSSEVYCOMETGAGNTLV 254	CC Ciliophora; Cionidae; Ciona.	
Db	113 PSQECIORSRPHOLIYKDCSYYAIGKRSSETTYTDFPNSSEVYCOMETGAGNTLV 254	CX NCBI_TaxID=7719;	
Qy	255 QARLDGSTNFTWDQYKAGFNLREFWLGNDKHLLTKSKEMLIJDDEFGVLYA 314	RT SEQUENCE FROM N.A.	
Db	173 QARLDGSTNFTWGKWDYKAGFNLREFWLGNDKHLLTKSKEMLIJDDEFGVLYA 232	RA Hotta K.; Takahashi H.; Asakura T.; Saitoh B.; Takatori N.; Satou Y.; RA "Characterization of Brachyury downstream notochord genes in the Ciona intestinalis embryo.";	
Qy	315 LYQDFYYVANEFLKYRLHVNGTAGDALRSHRMHDRLFPTPDRNDRYPSNCGLY 374	RT Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.	
Db	233 VDQDFYYVANEFLKYRLHVNGTAGDALRSHRMHDRLFPTPDRNDRYPSNCGLY 292	RL EMBL: AB036349; BABC626.1; -	
Qy	375 YSSGMWFDACLSANLNGKYNNQRYGVNRGIFWGTPGVSCAHPGKPFPRCAKMRP 434	DR HSSP: P02671; IPI2D;	
	SQ SEQUENCE 652 AA; MW: 73252 MW; A492BA325162FOEC CRC64;	DR InterPro: IPR00218; Fibrinogen_C; 1;	

Query Match	26.0%	Score 618.5;	DB 5;	Length 652;				
Best Local Similarity	43.0%	Pred. No. 2.9e-33;						
Matches	120;	Conservative	53;	Mismatches 91;	Indels 15;	Gaps 6;		
RESULT 6								
C9D2C2		PRELIMINARY:						
Q9D2C2;		PRT;	496 AA.					
AC Q9D2C2;								
DR 01-JUN-2001 (TREMBLrel. 17, Created)								
DR 01-JUN-2001 (TREMBLrel. 17, Last sequence update)								
DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)								
DR 1 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031cc0E18, full insert sequence (Argipointerin 2)								
DR AGPT2.								
OS Mus musculus (Mouse);								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus;								
OC NCBI TaxID:10090;								
RN [1];		SEQUENCE FROM N.A.						
RC STRAIN-C57BL/6J; TISSUE=Ovary and Uterus;								
MEDLINE=21G85666; PubMed=1127851;								
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa C., Hara A., Fukunishi Y., Konno H., Adachi J., Furukawa S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I., Saito T., Ozaki Y., Gotohori T., Bono H., Kasaiwa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Battalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuen P., Lewis S., Matsuo Y., Nishida I., Pesole G., Quackenbush J., Schiralli L.M., Staabli F., Suzuki R., Tonita M., Wagner L., Washio C., Saka K., Okido T., Furukawa M., Aono H., Baldarelli R., Barth G., Blake C., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garboldi M., Gustincich S., Hill D., Hoffmann M., Hurni D.A., Kamiya M., Lee N.H., Lyons P., Marchionni E., Mashima J., Mazzarelli C., Montaudo N., Nordone P., Ring B., Rinewald M., Rodriguez I., Sakamoto N., Suzuki H., Sato K., Schoenbach C., Seya T., Shiba T., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.-H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Kawaji H., Kohtsuki S., Hayashizaki Y.;								
RA "Functional annotation of a full-length mouse cDNA collection."; RT Nature 409:685-690 (2001).								
RN [2];		SEQUENCE FROM N.A.						
RP STRAUSBERG R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.								
RL 13;								
RP SEQUENCE FROM N.A.								
RC STRAIN-C57BL/6J; TISSUE=Head;								
RC MEDLINE=22254683; PubMed=12466851;								
RA The FANTOM Consortium;								
RA The RIKEN Genome Exploration Research Group Phase I & II Team;								
RA "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";								
RA Nature 420:563-573 (2002).								
RA SEQUENCE FROM N.A.								
RC STRAIN-C57BL/6J; TISSUE=Head;								
RC MEDLINE=AK013860; PubMed=173 (2002).								
DR EMBL: BC027216; AAC27216;								
DR EMBL: AK048122; BAC03396.1; -;								
DR HSSP: P02676; 1F2D;								
DR NGD: NGI:1202890; Agpt2.								
DR InterPro: IPR00218; Fibronogen_C.								
DR Pfam: PF00147; fibrinogen_C.								
DR SMART: SM00186; FBG_1.								
DR PROSITE: PS00544; FIBRIN_AGC_DOMAIN; 1.								
FT NON_TER 1.								
SQ SEQUENCE 220 AA; 25758 MW; 4160FAE727F3ED06 CRC64;								
Query Match	25.0%	Score 593.5;	DB 5;	Length 220;				
Best Local Similarity	49.8%	Pred. No. 3.5e-32;						
Matches	107;	Conservative	42;	Mismatches 61;	Indels 5;	Gaps 3;		
CY 227 YRVTIPKNSSEFYCDMEYGGTYLQLRGSTNFRTWQYKAGSKNKFREFFIGN 2856;								
DR 4 YEIKPA-TDEWVAYCDMEYGGTYLQERGGENFRNKAYANGDKDHWKGL 62								
CY 287 DKHHLT--KSKEMLRIDLDEQNGVELAYUQDQFYVANEFLKVRHGVNGNTAGAL 342								
DR 63 ERMHHLTSNSRSLKCRIDIIDWNVHYAEYEY-FRVREGEKSYCLAKKPSSTAGAL 122								
CY 344 RPKGHNHDKFETTDKDNDRYPGCGLYSSCNWFACLSANLNKGYYHOKYGRYN 403								
DR 123 NYGENINHMDAFTFDRDNGGALGNCGRYRSWNFKACAFANLNQNYTGFYGRQN 182								
CY 404 GIEFKGTPGVSSEAHPGYKSSFEKAMINPKHEK 433								
DR 183 GIYWGZWKLSRSRNSA-RYSKVVDMVKPLNFE 216								

6: LPPLTIO-PKOFSSR1EEVFKEVNLSKKSQDCXQLOADNGDPRGNGLL-PSTG 120
 Query Match 22.1%; Score 526; DB 11; Length 496;
 Best Locca: Similarity 32.9%; Pred. No. 3.2e-27;
 Matches 127; Conservative 66; Mismatches 153; Indels 40; Gaps 9;
 DR 142 LTDVEAVLNQTCITRL-----BLQJQHSISINKERQILQQTSE-NKLQKNNSFI-----191
 CY 121 APGEVGDNRVRLEJESEVNLK-SSELKRAKEEINVHLGR-----EKLNVLNPNNIENY 172

Db	192 -----EQKVLDEMEGHSEQEQLQSMKEQKDILQVLYSKQSSEVIDLEKLVATVYN.. SL 24.3	Qy	353 LKEFTTPDKNDRYPSGNCGLYSSGWWFACLSANLNGKYHOKYRGVR-NGIFWGTWP 41;
Qy	173 VDSKVANLTENVNS-DGCKCSKPSQEQIQSRPVGHLIYKDCSDYIAIGRSSETTYRV-TPD 23.2	Db	334 ---FSKDAKDNC1C-KCSQMLTGGWWFACGSPLNNGHYP_P.RQNNNNFNGTKWYKK 38.9
Db	244 LQKQHDLMETVNSLTMMSPPNSVAIRKEEETFRDCAEFKSGLTTSGYTL-TPP 30.3	Qy	412 GYSEAHPGGKSSFEAKM0IRPKHF 43.7
Qy	233 PKNSSEVYCMTMETGGWTVLQALIJDGSTNTTRTWOQKAGGNLEREFWLNQDKHHL 29.2	Db	390 G-----SGY--SLKATTMMIRPADF 40.7
Db	304 NSTEELKAYCADCMDVGGGWTVLQHEDGSDFORTWKEYKEGFSPLSEWLGNEFVSQL 36.3	RESULT 8	
Qy	293 TRSKEMILRIDEDENGVELAYLQYDVFYANEFLYKRYHGNVNTAGDLRKNKHYNHD 35.2	ID Q9DER0	PRELIMINARY;
Db	364 TQHRYVLLKQJKOWGENEASLHYHFLAGEESNYRILTGTTGTAGKISS-SQPGSD- 42.2	ID Q9DER0	PRT; 441 AA.
Db	353 LKEFTTPDKNDRYPSGNCGLYSSGWWFACLSANLNGKYHOKYRGVR-NGIFWGTWP 41.1	AC D7-	01-MAR-2001 (TREMBLrel. 16; Created)
Qy	423 ---FSKDAKDNC1C-KCSQMLTGGWWFACGSPLNNGHYP_P.RQNNNNFNGTKWYKK 37.8	AC D7-	01-MAR-2001 (TREMBLrel. 16; Last sequence update)
Db	412 GYSEAHPGGKSSFEAKM0IRPKHF 43.7	AC D7-	01-DEC-2001 (TREMBLrel. 19; Last annotation update)
Qy	479 G-----SGY--SLKATTMMIRPADF 49.6	DN ANGIOPOIETIN-2C.	
Db	RESULT 9		
Q9DER0		OS Gallus gallus (Chicken).	
RN 1		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RP SEQUENCE FROM N.A.		Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
RX MEDLINE=23422311; PubMed=10964717;		CC Gallus.	
RA Mezquita J., Mezquita P., Montserrat P., Yezquita B., Francone V.,		NCBI_TaxID=9031;	
RA Vilagrassa X., Mezquita C.;		RN [1]	
RT "Genomic structure and alternative splicing of chicken angiopeptin-2."		RP SEQUENCE FROM N.A.	
RT 2.";		RX MEDLINE=23422311; PubMed=10964717;	
DE Bicchem. Biophys. Res. Commun. 275:643-651 (2000).		RA Mezquita J., Mezquita P., Montserrat P., Yezquita B., Francone V.,	
CN EMBL; AJ28779; CAC08176.1; -.		RA Vilagrassa X., Mezquita C.;	
DR HSSP; P02671; IFZD.		RT "Genomic structure and alternative splicing of chicken angiopeptin-2."	
DR InterPro: IPR002181; Fibrinogen_C; 1.-		RT 2.";	
DR SMART: SMCC186; FBG; 1.		RL Biochem. Biophys. Res. Commun. 275:643-651 (2000).	
DR PROSITE: PS00514; FIBRIN AG C_DOMAIN; 1.		DR EXBL; AJ28778; CAC08175.1; -.	
DR Sequence: 441 AA; 50472 MW; DC8127FECE34E2 CRC64;		DR HSSP; P02671; IFZD.	
SQ Score 524; Length 441;		DR InterPro: IPR002181; Fibrinogen_C; 1.-	
Query Match 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		DR SMART: SMCC186; FBG; 1.	
RT 2.";		DR PROSITE: PS00514; FIBRIN AG C_DOMAIN; 1.	
RT "Genomic structure and alternative splicing of chicken angiopeptin-2."		DR Sequence: 407 AA; 46687 MW; 8963BA0B8C7A4:C CRC64;	
RT 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		Qy 233 PKNSSEVYCMTMETGGWTVLQARDGSTNTTRTWOQKAGGNLEREFWLNQDKHHL 29.2	
SQ Score 524; Length 407;		Db 249 NSAQEKAYCDESNGGWTLQRREDGSDFEHRTKEYIGF3PAGEWLGNEFVSQI 3CB	
Query Match 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		Db 197 NETVHNLLMTSTPNSAKNTZAKEOIS-----FQDAAEAKSGLTSGITLTFP 24.8	
RT 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		Qy 253 TKSKEMLRILEDENGVELAYLQYDVFYANEFLYKRYHGNVNTAGDLRKNKHYNHD 35.2	
SQ Score 524; Length 407;		Db 309 TNQKRYVLLIKDQWEGNEATLYDQFYLANEQQYRHHGLTGTAGKISS-SOPGND- 36.7	
Query Match 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		Db 353 LKEFTTPDKNDRYPSGNCGLYSSGWWFACLSANLNGKYHOKYRGVR-NGIFWGTWP 41.1	
RT 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		Db 368 ---FSKDAKDNC1C-KCSQMLTGGWWFACGSPLNNGHYP_P.RQNNNNFNGTKWYKK 42.3	
RT 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		Qy 412 GYSEAHPGGKSSFEAKM0IRPKHF 43.7	
RT 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		Db 424 G-----SGY--SLKATTMMIRPADF 44.1.	
RT 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		RESULT 9	
RT 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		Q9DER2	PRELIMINARY;
RT 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		ID Q9DER2	PRT; 493 AA.
RT 22.0%; Best Local Similarity 38.3%; Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 13;		AC Q9DER2;	

DT	C1-MAR-2001 (TREMBLrel. 16; Created)	RA	Mezquita J., Mezquita B., Pau M., Mezquita C.;
DT	01-MAR-2001 (TREMBLrel. 16; Last sequence update)	RT	"Characterization of a novel form of angiopoietin-2 (Ang-2B) and expression of VEGF and angiopoietin-2 during chicken testicular development and regression."
DE	Angiopoietin-2A.	RU	
GN	ANGIOPETIN-2.	RL	Biochem. Biophys. Res. Commun. 260:492-498(1999).
CS	Gallus gallus (Chicken).	EMBL	AI:131923; CAB5200.1; -.
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galiformes; Phasianidae; Phasianinae; OC	DR	HSSP: F02671; 1F2D.
OC	Archosauria; Aves; Neognathae; Galiformes; Phasianidae; Phasianinae; OC	InterPro	IPIR002181; Fibroinogen_C.
CX	KCBI_TaxID=9031;	DR	InterPro; PF00147; Fibroinogen_C; -.
RN	[1]	SMART	SM00186; FBG; 1.
RP	SEQUENCE FROM N.A.; PubMed=1036417;	PROSITE	PS00514; FIBRINAG_C_DCM4-IN; 1
RX	MEDLINE=042231; PubMed=1036417;	SEQUENCE	E13C03D0/E410013 CRC64;
RA	Mezquita J., Mezquita B., Montserrat P., Mezquita C., Mezquita V., Mezquita X., Mezquita C.;	Query Match	Score 523; DB 13; Length 407;
RT	"Genomic structure and alternative splicing of chicken angiopoietin-2".	Best Local Similarity	38.3%; Pred. No. 4e-27;
RL	Biochem. Biophys. Res. Commun. 275:643-651(2002);	Matches	36; Gaps 10;
DR	EMBL: AJ289777; CAC08174; -.	Conservative	35; Mismatches 120; Indels 36;
DR	HSSP; P02671; 1F2D.	Indels	36;
DR	InterPro; IPIR002181; Fibroinogen_C; -.	Score	523;
DR	PF00147; Fibroinogen_C; 1..	Pred. No.	4e-27;
DR	SMART; SM00186; FBG; 1.	Best Local Similarity	38.3%; Pred. No. 4e-27;
DR	PROSITE; PS00514; FIBRINAG_C_DOMAIN; 1.	Matches	36; Gaps 10;
SC	SEQUENCE 493 AA; 56393 MW; BC-A21F90172F6DA CRC64;	Conservative	35; Mismatches 120; Indels 36;
Query Match	Score 524; DB 13; Length 493;	Score	523;
Best Local Similarity	38.3%; Pred. No. 4e-27;	Pred. No.	4e-27;
Matches	36; Gaps 10;	Best Local Similarity	38.3%; Pred. No. 4e-27;
Conservative	35; Mismatches 120; Indels 36;	Matches	36; Gaps 10;
Indels	36;	Indels	36;
QY	127 CNVRELESEVNKLSELQKAKKEEINVHLGR-----LEK-LNLVMMNI----ENVV 173	QY	127 CNVRELESEVNKLSELQKAKKEEINVHLGR-----LEK-LNLVMMNI----ENVV 173
DB	189 EKVLFMEDKFLQLQSKSIKEEDQOQLVLVRQSNTIEELQLQTATVNSVQKQGD; 248	DB	189 EKVLFMEDKFLQLQSKSIKEEDQOQLVLVRQSNTIEELQLQTATVNSVQKQGD; 248
QY	174 DSKVAN-LTEVNSLDGKCKSKCPSEQIQCRSPVQHLYIKDCSDYYAIGKRSSETYRVTFO 232	QY	174 DSKVAN-LTEVNSLDGKCKSKCPSEQIQCRSPVQHLYIKDCSDYYAIGKRSSETYRVTFO 232
DB	249 MEVTRNLMTSPNSAKONFIKEQIS-----EKDCAAEFKSGLTTSGYT-ZTP 300	DB	249 MEVTRNLMTSPNSAKONFIKEQIS-----EKDCAAEFKSGLTTSGYT-ZTP 300
QY	233 PKNSSEVCDMNETGGWTVLQALDGSINFTRWQDIIKAGGNLRRFWLQNDKIHLL 292	QY	233 PKNSSEVCDMNETGGWTVLQALDGSINFTRWQDIIKAGGNLRRFWLQNDKIHLL 292
DB	301 NSAQERKAYCDMESNGGWTMLQREDGSDFEHRPTWEKIGGDPAGEYWLNNEFVSL 360	DB	301 NSAQERKAYCDMESNGGWTMLQREDGSDFEHRPTWEKIGGDPAGEYWLNNEFVSL 360
QY	293 TSKEMILRILEDENGVELYALYDQFYVANEFLKYLHVNYNTAGDALFRNKHYHD 352	QY	293 TSKEMILRILEDENGVELYALYDQFYVANEFLKYLHVNYNTAGDALFRNKHYHD 352
DB	361 NYQRKAVRKIIKQWGENEYTYIYQPKFLANEQTRHILKGFTSTAGKTSISQPGND- 419	DB	361 NYQRKAVRKIIKQWGENEYTYIYQPKFLANEQTRHILKGFTSTAGKTSISQPGND- 419
QY	353 LKEFFTDPDKNDRDYFSQNCGLYYSSGWWFADCLSANLNGKYYHQYRGYR-NGIFWGTWP 411	QY	353 LKEFFTDPDKNDRDYFSQNCGLYYSSGWWFADCLSANLNGKYYHQYRGYR-NGIFWGTWP 411
DB	420 --FSTKDADDKCIC-KCSQMLTGWWFADG2SNLNGKYYPLQNNNNKFNGKRYWIK 475	DB	420 --FSTKDADDKCIC-KCSQMLTGWWFADG2SNLNGKYYPLQNNNNKFNGKRYWIK 475
QY	412 GVSEAHPGGYKSSEKAQMNTRPKF; 437	QY	412 GVSEAHPGGYKSSEKAQMNTRPKF; 437
DB	476 G-----SGY--SSRATTNNMRPADF 493	DB	476 G-----SGY--SSRATTNNMRPADF 493
RESULT 13		RESULT 11	
ID	Q9PU54	ID	Q3C25
AC	Q9PU54;	PRELIMINARY;	PRELIMINARY;
DT	01-MAY-2000 (TREMBLrel. 13; Created)	PRT;	314 AA.
ET	01-MAY-2000 (TREMBLrel. 13; Last sequence update)	AC	Q8YC25;
DT	01-MAY-2000 (TREMBLrel. 17; Last annotation update)	DT	01-MAR-2002 (TREMBLrel. 20; Created)
DE	Angiopoietin-2B (Ang-2B).	DT	01-MAR-2002 (TREMBLrel. 20; Last sequence update)
GN	ANGIOPETIN-2.	DT	01-OCT-2002 (TREMBLrel. 22; Last annotation update)
OS	Gallus gallus (Chicken).	DE	Similar to fibroinogen-like 1.
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bitheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; OX	GN	EG1.
NCBI_TaxID	10909;	OS	Mus musculus (Mouse).
RN	[1]	CC	Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bitheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; OX
RP	SEQUENCE FROM N.A.	NCBI_TaxID	10909;
RC	TISSUE=Liver;	RP	SEQUENCE FROM N.A.
RA	Strausberg R.;	RC	TISSUE=Liver;
RL	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.	RA	Strausberg R.;
DR	EMBL; ACC21246; AN21946.1; -.	RL	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR	InterPro; IPIR002181; Fibroinogen_C; 1..	DR	EMBL; ACC21246; AN21946.1; -.
DR	PFAM; PF00147; Fibroinogen_C; 1..	DR	InterPro; IPIR002181; Fibroinogen_C; 1..
DR	SMART; SM00186; FBG; 1.	DR	PFAM; PF00147; Fibroinogen_C; 1..
DR	PROSITE; PS00514; FIBRINAG_C_DOMAIN; 1.	DR	SMART; SM00186; FBG; 1.
SQ	SEQUENCE 314 AA; 36439 MW;	DR	PROSITE; PS00514; FIBRINAG_C_DOMAIN; 1.
QY	110 GRNGJLPLSTGAPEGVGDNRVRELESEVNKLSELKNAKEE-NVLMGRLEKLNLYNN 168	SEQUENCE	314 AA; 36439 MW;
QY	110 GRNGJLPLSTGAPEGVGDNRVRELESEVNKLSELKNAKEE-NVLMGRLEKLNLYNN 168	Query Match	21.8%; Score 518.5; DB 11; Length 314;
OX		Best Local Similarity	37.0%; Pred. No. 5.7e-27;
RN		Matches	126; Conservative 42; Mismatches 116; Indels 57; Gaps 12;
RC	SEQUENCE FROM N.A.	RC	SEQUENCE FROM N.A.
RX	STRAIN= Hubbard White Mountain;	RP	SEQUENCE FROM N.A.
RX	MEDLINE=99333704; PubMed=10403795;	RC	SEQUENCE FROM N.A.

Db	17	GREGNALESESCURE---CVRIRACYFQOLETRVKQQOTMIQLIHEK.-EVCFLDKGS 69	RESULT 13
Qy	169	ENYYDSKVANLTIVVNCSLDGCKSKCPSEQC1OSRPFVQHLYKDSDYAAIGRSSETYR 228	095641 PRELIMINARY; PRT; 49; AA.
Db	7C	ENSFD-----LGKRO-----YADCSEYNDGFKSGYK 200	AC 095841 ID; 49; AA.
Cy	229	VTPDEKNSSEPEVYCDMETNGGGATVQARLDGSTNFTRTWCDFKAGFGNL--RREFWFLG 285	AC 095841 ID; 49; AA.
Db	101	IKPLQSLAESVYCDMSD-GGNTVQIQRSDGSNFNRCNDENGFRVONGEGLW 159	DT 01-MAY-1999 [TREMBLrel. 1C, Created]
Qy	286	NDKHLALTSKEMILRIDLDEPGVELTALYDQFVANEFLKYL-HVGNYNTGAGDLRF 345	DT 01-CCT-2002 [TREMBLrel. 1C, Last sequence update]
Db	160	KNINNLTL-QGDYTLKIDLTDFFKNSSFQYQOSPKVGDKKFELNGEYSGTAGDSLGS 219	DT 01-MAR-2003 [TREMBLrel. 22, Last annotation update]
Qy	346	NCH-----YNHDOLKEFTTPDKONDRTPSGNCGLYSSGKWFACLSANLNGYYHOKYR 399	DE Angiopoietin Y1 (D595C2.2); Angiopoietin-related protein 1 precursor;
Db	220	TPHPFQVQWASHQRMKESTWDRDNY-QNCNAEEQSSXWFRCHSANLNGYYHRSYR 276	DE 0595C2.2 OR ARPI.
Qy	400	G-VRNGLIFACTWPGVSEAHPGVYKSSFXEAKMMPRKHKFP 439	GN Homo sapiens (Human).
Db	279	AETDNGVWVYTW-----HGWWYSLKSVMKIRPSDFP 311	OS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; OC Primates; Catarrhini; Hominidae; Homo.
Db			NCBI TaxID:9606; NCBI_TaxID:9606; [1]
Qy			RN SEQUENCE FROM N.A.
Db			RC TISSUE=Heart; MEDLINE=99148929; PubMed=10025962;
Qy			RA Kim I., Koak H.J., Ahn J.E., So J.N., Liu M., Koh G.Y.; "Molecular cloning and characterization of a novel angiopoietic family protein, angiopoietin-3." PEBS Lett. 443:353-356(1999).
Db			RL [2]
Qy			RN SEQUENCE FROM N.A.
Db			RA Cobley V.; Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
Qy			RL [3]
Db			RN SEQUENCE FROM N.A.
Qy			RC TISSUE=Placenta; MEDLINE=99148930; PubMed=10025963;
Db			RA Ota T., Niishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K., Yamamoto J., Sugano S., Isogai T.; "HRI human cDNA sequencing project." RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
Qy			RA Cobley V.; Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
Db			RL [4]
Qy			RN SEQUENCE FROM N.A.
Db			RC TISSUE=Placenta; MEDLINE=99148931; PubMed=10025964;
Qy			RA Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T., Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Matsusho Y., Suda T.; "Molecular cloning and characterization of novel angiopoietin-related protein (ARP4)." RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
Db			DR AF127253; ADD19608; 1/-.
Qy			RA "Molecular cloning and characterization of novel angiopoietin-related protein (ARP4)." DR AF127253; ADD19608; 1/-.
Db			DR AL335520; CAC13169; 1/-.
Qy			RA "Molecular cloning and characterization of novel angiopoietin-related protein (ARP4)." DR AB056476; BAB0691; 1/-.
Db			DR HSSP; P02611; 1PZD.
Qy			DR Genew; HGNC:489; ANGPTL1.
Db			DR InterPro; IPR022181; Fibrirogen_C.
Qy			DR Pfam; PF03147; Fibrirogen_C; 1.
Db			DR SMART; SM00186; FBG; 1.
Qy			DR PROSITE; PS00514; FBIRN_AGC_DOMAIN; 1.
Db			KW Signal; 1 23 POTENTIAL.
Qy			FT CHAIN 24 491 POTENTIAL.
Db			SO SEQUENCE 491 AA; 56719 MW; 3C4DBBDDF6CF7E99 CRC64;
Qy			Query Match Score 21.3%; Best Local Similarity 44.6%; Pred. No. 3.9e-26; Matches 107; Conservative 25; Xismatches 93; Indels 20; Gaps 6;
Db			Query Match Score 21.3%; Best Local Similarity 44.6%; Pred. No. 8.1e-26; Matches 13; Conservative 81; Xismatches 137; Indels 138; Gaps 15;
Qy			Cy 47 GKCEEGCECPYQVSUPPLTCJP-----KQFSR1EEVP--KEVONLKIEVNSIKKSCQ 97
Db			Db 42 GK-EPEAKCAY-FLVEPQTGPICVNTKQDASTIKOMTRMLENU-KDVLRSQRKREID 100
Qy			Cy 98 DCKLADDNGDPGRNSSLPLSTGAPGEVGDNVRPLESENKLSELKAKEE-NVLHSLR 157
Db			Db 101 VLQLVVDVGN-----IVNEVKLLRKESRNMNSRVQLMQ 136
Qy			Cy 158 L-----EKLNVNNNNNNVV-----DSKVNLTFVWS-----L 187
Db			Db 137 LLHEITRKDRNSLEISQLENKLNATMTRYRELKVASLTDLVNNQSVMITL 196
Qy			Cy 188 DGKCSKCPSEQIQSRP-----VOHL-----

Db	197	EDQURIFRQQDTEVSPPLVCVYQHPIPNSSQQTPTGLGGNEICRDGYPRDLMPPPFDLA	256	QY	416	AHPGGKKSSEAKMIRPGRIF	437
Cy	209	-----IYKODSDYYAIGRSSETYRVTPPKSSFEYVCDMETMGG	249	Db	228	--SGI--SLRATMMIRADF	244
Db	257	TSPTRKSPFQKIPPFINEPFPKIDQCAKEAGHSYGSIMIKKPNSKGMLQMCENSLSLPG	316	RESULT 15			
Cy	250	GWTYQLQRDGSTNFTRTQCYKAGFGNLREFW-GNDKHILTKSKEMILRIDIEDFNG	309	Q90219	PRELIMINARY:	PRT;	513 AA.
Db	257	GWTYQLQRDGSTNFTRTQCYKAGFGNLREFW-GNDKHILTKSKEMILRIDIEDFNG	309	ID	Q90219		
Cy	317	GWTYQLQRDGSTNFTRTQCYKAGFGNLREFW-GNDKHILTKSKEMILRIDIEDFNG	309	AC	Q90219,		
Db	316	GWTYQLQRDGSTNFTRTQCYKAGFGNLREFW-GNDKHILTKSKEMILRIDIEDFNG	309	DT	01-DEC-2001	(TREMBrel. 19, Created)	
Cy	316	GWTYQLQRDGSTNFTRTQCYKAGFGNLREFW-GNDKHILTKSKEMILRIDIEDFNG	309	DT	01-MAR-2001	(TREMBrel. 19, Last sequence update)	
Db	377	KKYAEYSSRFLEPESEFYRLRLCTYQGAGSMNW----HNKGQFTTLDRKDY-AG	433	DT	01-MAR-2003	(TREMBrel. 23, Last annotation update)	
Cy	370	NCGLYYSSKKWFDCISANLNGKHYH-QKRYGV-RNGIFWGT-PGVSSEAHPGGYKSSEKE	427	DE		Angiopoietin-1.	
Db	431	NCGLYYSSKKWFDCISANLNGKHYH-QKRYGV-RNGIFWGT-PGVSSEAHPGGYKSSEKE	427	GN		ANGPT1, CR_ANG1.	
Cy	428	AKMIRP	434	OS		Brachydanio rerio (Zebrafish) (Danio rerio).	
Db	483	VQMIKP	489	RX		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Cy	483	VQMIKP	489	RX		Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
Db	483	VQMIKP	489	RX		Cyprinidae; Danio.	
Cy	111			RX		NCBI_TaxID:7955;	
Db	483	VQMIKP	489	RX		SEQUENCE FROM N.A.	
Cy	111			RX		MEDLINE=21391693; PubMed=11500955;	
Db	483	VQMIKP	489	RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Cy	111			RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Db	483	VQMIKP	489	RX		Dev. Dyn. 296(2):470-474 (2001).	
Cy	111			RX		EMBL; AF319602; AAC833471;	
Db	483	VQMIKP	489	RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Cy	111			RX		Interozo; IPROC0181; Fibrorogen_C.	
Db	483	VQMIKP	489	RX		SMART; SM00186; FBG1_2.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		SEQ ID: 58365 MW;	
Db	483	VQMIKP	489	RX		6627777739847DEB GRC64;	
Cy	111			RX		SEQUENCE FROM N.A.	
Db	483	VQMIKP	489	RX		MEMLINE=21391693; PubMed=11500955;	
Cy	111			RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Db	483	VQMIKP	489	RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Cy	111			RX		Dev. Dyn. 296(2):470-474 (2001).	
Db	483	VQMIKP	489	RX		EMBL; AF319602; AAC833471;	
Cy	111			RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Db	483	VQMIKP	489	RX		Interozo; IPROC0181; Fibrorogen_C.	
Cy	111			RX		SMART; SM00186; FBG1_2.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		SEQ ID: 58365 MW;	
Cy	111			RX		6627777739847DEB GRC64;	
Db	483	VQMIKP	489	RX		SEQUENCE FROM N.A.	
Cy	111			RX		MEMLINE=21391693; PubMed=11500955;	
Db	483	VQMIKP	489	RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Cy	111			RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Db	483	VQMIKP	489	RX		Dev. Dyn. 296(2):470-474 (2001).	
Cy	111			RX		EMBL; AF319602; AAC833471;	
Db	483	VQMIKP	489	RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Cy	111			RX		Interozo; IPROC0181; Fibrorogen_C.	
Db	483	VQMIKP	489	RX		SMART; SM00186; FBG1_2.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		SEQ ID: 58365 MW;	
Db	483	VQMIKP	489	RX		6627777739847DEB GRC64;	
Cy	111			RX		SEQUENCE FROM N.A.	
Db	483	VQMIKP	489	RX		MEMLINE=21391693; PubMed=11500955;	
Cy	111			RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Db	483	VQMIKP	489	RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Cy	111			RX		Dev. Dyn. 296(2):470-474 (2001).	
Db	483	VQMIKP	489	RX		EMBL; AF319602; AAC833471;	
Cy	111			RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Db	483	VQMIKP	489	RX		Interozo; IPROC0181; Fibrorogen_C.	
Cy	111			RX		SMART; SM00186; FBG1_2.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		SEQ ID: 58365 MW;	
Cy	111			RX		6627777739847DEB GRC64;	
Db	483	VQMIKP	489	RX		SEQUENCE FROM N.A.	
Cy	111			RX		MEMLINE=21391693; PubMed=11500955;	
Db	483	VQMIKP	489	RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Cy	111			RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Db	483	VQMIKP	489	RX		Dev. Dyn. 296(2):470-474 (2001).	
Cy	111			RX		EMBL; AF319602; AAC833471;	
Db	483	VQMIKP	489	RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Cy	111			RX		Interozo; IPROC0181; Fibrorogen_C.	
Db	483	VQMIKP	489	RX		SMART; SM00186; FBG1_2.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		SEQ ID: 58365 MW;	
Db	483	VQMIKP	489	RX		6627777739847DEB GRC64;	
Cy	111			RX		SEQUENCE FROM N.A.	
Db	483	VQMIKP	489	RX		MEMLINE=21391693; PubMed=11500955;	
Cy	111			RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Db	483	VQMIKP	489	RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Cy	111			RX		Dev. Dyn. 296(2):470-474 (2001).	
Db	483	VQMIKP	489	RX		EMBL; AF319602; AAC833471;	
Cy	111			RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Db	483	VQMIKP	489	RX		Interozo; IPROC0181; Fibrorogen_C.	
Cy	111			RX		SMART; SM00186; FBG1_2.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		SEQ ID: 58365 MW;	
Cy	111			RX		6627777739847DEB GRC64;	
Db	483	VQMIKP	489	RX		SEQUENCE FROM N.A.	
Cy	111			RX		MEMLINE=21391693; PubMed=11500955;	
Db	483	VQMIKP	489	RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Cy	111			RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Db	483	VQMIKP	489	RX		Dev. Dyn. 296(2):470-474 (2001).	
Cy	111			RX		EMBL; AF319602; AAC833471;	
Db	483	VQMIKP	489	RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Cy	111			RX		Interozo; IPROC0181; Fibrorogen_C.	
Db	483	VQMIKP	489	RX		SMART; SM00186; FBG1_2.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		SEQ ID: 58365 MW;	
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Db	483	VQMIKP	489	RX		MEMLINE=21391693; PubMed=11500955;	
Cy	111			RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Db	483	VQMIKP	489	RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Cy	111			RX		Dev. Dyn. 296(2):470-474 (2001).	
Db	483	VQMIKP	489	RX		EMBL; AF319602; AAC833471;	
Cy	111			RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Db	483	VQMIKP	489	RX		Interozo; IPROC0181; Fibrorogen_C.	
Cy	111			RX		SMART; SM00186; FBG1_2.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		SEQ ID: 58365 MW;	
Cy	111			RX		6627777739847DEB GRC64;	
Db	483	VQMIKP	489	RX		SEQUENCE FROM N.A.	
Cy	111			RX		MEMLINE=21391693; PubMed=11500955;	
Db	483	VQMIKP	489	RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Cy	111			RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Db	483	VQMIKP	489	RX		Dev. Dyn. 296(2):470-474 (2001).	
Cy	111			RX		EMBL; AF319602; AAC833471;	
Db	483	VQMIKP	489	RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Cy	111			RX		Interozo; IPROC0181; Fibrorogen_C.	
Db	483	VQMIKP	489	RX		SMART; SM00186; FBG1_2.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		SEQ ID: 58365 MW;	
Db	483	VQMIKP	489	RX		6627777739847DEB GRC64;	
Cy	111			RX		SEQUENCE FROM N.A.	
Db	483	VQMIKP	489	RX		MEMLINE=21391693; PubMed=11500955;	
Cy	111			RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Db	483	VQMIKP	489	RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Cy	111			RX		Dev. Dyn. 296(2):470-474 (2001).	
Db	483	VQMIKP	489	RX		EMBL; AF319602; AAC833471;	
Cy	111			RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Db	483	VQMIKP	489	RX		Interozo; IPROC0181; Fibrorogen_C.	
Cy	111			RX		SMART; SM00186; FBG1_2.	
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Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		SEQ ID: 58365 MW;	
Cy	111			RX		6627777739847DEB GRC64;	
Db	483	VQMIKP	489	RX		SEQUENCE FROM N.A.	
Cy	111			RX		MEMLINE=21391693; PubMed=11500955;	
Db	483	VQMIKP	489	RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Cy	111			RX		"Isolation and expression analysis of three zebrafish angiopoietin genes."	
Db	483	VQMIKP	489	RX		Dev. Dyn. 296(2):470-474 (2001).	
Cy	111			RX		EMBL; AF319602; AAC833471;	
Db	483	VQMIKP	489	RX		ZFIN; ZDB-GENE-010811-2; argip1.	
Cy	111			RX		Interozo; IPROC0181; Fibrorogen_C.	
Db	483	VQMIKP	489	RX		SMART; SM00186; FBG1_2.	
Cy	111			RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Db	483	VQMIKP	489	RX		PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.	
Cy	111			RX		SEQ ID: 58365 MW;	
Db	483	VQMIKP	489	RX		6627777739847DEB GRC64;	
Cy	111			RX		SEQUENCE FROM N.A.	
Db	483	VQMIKP	489	RX		MEMLINE=21391693; PubMed=11500955;	
Cy	111			RX		Rham V.N.; Roman B.L.; Weinstein B.M.;	
Db	483	VQMI					

W d Nov 5 17:46:57 2003

us-09-902-563-2.rspt

Page 8

Search completed: November 5, 2003, -6:47:34
Job time : 61.0176 secs

ED 19-NOV-1998.
 XX 15-MAY-1998; 98C0-CA00475.
 FF XX
 FR 10-OCT-1997; 97US-0061684.
 PR 15-MAY-1997; 97US-0046537.
 XX
 PA (LEVY//) LEVY G.
 XX
 PI Levy G;
 XX
 WPI; 1999-059687/05.
 DR N-PSDB; AA84139.
 XX
 P- Modulating immune coagulation - by using Fg12 antibodies and
 P- compounds used to treat conditions including graft rejection and
 P- foetal loss
 XX
 PS Claim 8; Page 66-67; 105pp; English.
 XX
 CC This is the amino acid sequence of human prothrombinase Fg12, as
 CC predicted from hFG12 DNA (see AAV84139). Fg12 is a 70 kDa
 CC transmembrane serine protease that has immune procoagulant activity.
 CC The invention provides a method for inhibiting immune coagulation by
 CC inhibiting the activity or expression of Fg12. The method can be
 CC used in vivo to treat a condition which requires a reduction in
 CC immune coagulation such as bacterial and viral infections, cancer,
 CC glomerulonephritis, a number of gastrointestinal diseases,
 CC allograft and xenograft rejection and foetal loss. An Fg12-specific
 CC antibody, an Fg12 antisense oligonucleotide, or a substance that
 CC affects prothrombinase activity of a Fg12 protein may be used to
 CC treat a condition requiring a reduction in procoagulant activity.
 CC A vaccine containing an Fg12 peptide or peptide is used for
 CC prevention of graft rejection or foetal loss (claimed).
 XX
 SC Sequence 439 AA;

Query Match Score 2378; DB 20; Length 439;
 Best Local Similarity 100.0%; Pred. NC_01-205; Mismatches 0; Indels 0; Gaps 0;
 Matches 439; Conservative 0; Pairs 2,1e-205;

Qy 1 MKLANYWLISSAVLTYGFIVANMTEETKDEKAKCOPVRLSRGKCEAECPYQVS 60
 Ds 2 : MKLANYWLISSAVLTYGFIVANMTEETKDEKAKCOPVRLSRGKCEAECPYQVS 60
 Qy 61 LPPLTQLPQFOSRVEEVKEYQNKEIVNSLKSQQCKLQADNGDPRGJLIPSTG 120
 Ds 61 LPPLTQLPQFOSRVEEVKEYQNKEIVNSLKSQQCKLQADNGDPRGJLIPSTG 120
 Cy 122 APGEVGSNRVRELEEVNLKLSSEKNAKEEINVLGEERLNLVNNNENYDSKYAL 180
 Ds 121 APGEVGSNRVRELEEVNLKLSSEKNAKEEINVLGEERLNLVNNNENYDSKYAL 180
 Qy 181 TFWNSLDGKCSKPCSQEQICSPRYQHLYKDSCYYA-TKRSSETYRVTPDKNSSEFV 240
 Ds 181 TFWNSLDGKCSKPCSQEQICSPRYQHLYKDSCYYA-TKRSSETYRVTPDKNSSEFV 240
 Cy 241 YCDMEITMGGMVTLQARLDSNTFTWDYKAGGNLRREFWLGNDK-HLILTSKEYL 300
 Ds 241 YCDMEITMGGMVTLQARLDSNTFTWDYKAGGNLRREFWLGNDK-HLILTSKEYL 300
 Cy 301 RIDLEDENGVEIAYLQDFYVANEFLKYRJHGNYNTAGDALRKNHNDLKPFETTD 360
 Ds 301 RIDLEDENGVEIAYLQDFYVANEFLKYRJHGNYNTAGDALRKNHNDLKPFETTD 360
 Cy 361 KNDYRPSGNGCGLYSSGMAEDACISANLNQKYYHOKYRGVRVNGIWFAGTWPGLPQG 420
 Ds 361 KNDYRPSGNCGLYSSGMAEDACISANLNQKYYHOKYRGVRVNGIWFAGTWPGLPQG 420
 Qy 421 YKSSPKEAKMIRPKIFKP 439
 Ds 421 YKSSPKEAKMIRPKIFKP 439

RESU-T 2
 AAW88236 standard; Protein; 432 AA.
 DE XX
 AC AAW88236;
 DT 15-MAR-1999 (First entry)
 DE XX
 DE XX
 KW Prothrombinase; Fg12; mouse; immune coagulation; antibody;
 KW inhibitor; infection; graft rejection; glomerulonephritis; cancer;
 KW gastrointestinal disease; foetal loss; therapy; vaccine.

Mus sp.
 XX
 Key
 FH Modified-site 172..174
 FT /label="Asn" is N-glycosylated 228..231
 FT Modified-site 256..259
 FT Modified-site 323..325
 FT Domain 213..439
 FT /note="tibrinogen related domain"
 XX
 WO9851335-A1.
 XX
 PN 19-NOV-1998.
 XX
 PR 15-MAY-1998; 98WO-CAG3475.
 XX
 PR 10-CC-1997; 97US-0061684.
 PR 15-MAY-1997; 97US-0046537.

LEVY // LEVY G.
 XX
 PI Levy G;
 XX
 NPZ; 1999-059687/05.
 DR AAV84140.
 XX
 PT Modulating immune coagulation - by using Fg12 antibodies and
 PT compounds, used to treat conditions including graft rejection and
 PT foetal loss
 XX
 PT Claim 8; Page 70-71; 105pp; English.
 XX
 CC This is the amino acid sequence of mouse prothrombinase Fg12, as
 CC predicted from f912 DNA (see AAV84140). Fg12 is a 70 kDa
 CC transmembrane serine protease that has immune procoagulant activity.
 CC The human Fg12 amino acid sequence is given in AAV86236. The
 CC invention provides a method for inhibiting immune coagulation by
 CC inhibiting the activity or expression of Fg12. The method can be
 CC used in vivo to treat a condition which requires a reduction in
 CC immune coagulation such as bacterial and viral infections, cancer,
 CC glomerulonephritis, a number of gastrointestinal diseases,
 CC allograft and xenograft rejection and foetal loss. An Fg12 specific
 CC antibody, an Fg12 antisense oligonucleotide, or a substance that
 CC affects prothrombinase activity of a Fg12 protein may be used to
 CC treat a condition requiring a reduction in procoagulant activity.
 CC A vaccine containing an Fg12 protein or peptide is used for
 CC prevention of graft rejection or foetal loss (claimed).
 XX
 Sequence 432 AA;

Query Match Score 1853.5; DB 20; Length 432;
 Best Local Similarity 77.7%; Pred. No. 3.9e-158;
 Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;

PT promoting or blocking neovascularisation, etc

XX XX NC0611659-A2.

PS XX 16-APR-1996.

CC XX 06-OCT-1995; 95WC-JS12935.

CC CC 06-APR-1995; 95US-C418555.

CC CC 07-OCT-1994; 94US-0319931.

CC CC 27-OCT-1994; 94US-0330261.

CC CC 02-DEC-1994; 94US-0348492.

CC CC 09-DEC-1994; 94US-03353503.

XX PR 17-JAN-1995; 95US-0373579.

SQ Sequence 496 AA:

```

Query Match Score 522; DB 17; Length 496;
Best Local Similarity 27.9%; Pred. No. 5.2e-38;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

```

QY 43 LERGKRE---EAGECPYCVSLPPL-----T:Q-LPKQSRIEVFKEVQN 94
Db 26 MDS:GRKCYQOHGSYTPEMCRSSSPVSNAQRDPSVORLQVLEN 95

Cy 85 LKE----IVNSLKKSCQQCKLQADNDPGRNGLLPSTGARGEWGDN--- 128

Db 86 IMENNTQWLMLDENTQDNMKEMYEIQNQAVON-----CTAMIEIGTNLNLC 134

Qy 129 -----RVRLESEV-----NKLUSSLEKAKREBINVLHGR--DEKL 161

Db 135 TAEQTRKLTDVEAQVLNCTTEELQLEHSLSNTKLEQQLDQTSBINKLQDQNSFJEEK 194

Qy 162 NLV-----NKNNNENYDVSQKVNLTTF-----v 183

Db 195 VLMEDKHITIQLQS:KEEKQ:Q:QVLYSKQNSNIELEKKVITATNNSYLQKCHDMT 254

Qy 184 VNLSDGKCSKCPSSQEQIGSRPVCHLJYKDCSDYYAIGRSSETRYTEDPPNSSFVFCO 243

Dc 255 VNNLJTMMSSTSNAKDPVAKEEQISFRDCAEVFKSGHTNGVLTLPNSTEEIKACD 3.4

Qy 244 METWGGWTVIQARLDGSTNFTRTHDYKAGFQGNREFFLGRDKIHLTKSKEMILID 303

Db 315 MEAGGGGTWITIQRREGPSVDFORTKEYKVYGFQNGPSGEVNLGNEFVSQLTNOQRYVLUKH 374

Cy 304 LEDEFGNVELVAJYDCPYVANEFLVKRJHVGRNYNTAGDALRFGHYNHDLKFETTPDKDN 363

Db 375 KDKMEGEAASLYIENFYISSEEFLVNRHKGKLGTLTAGK-SSISPGNC---ESTKDGN 430

Qy 364 DRYFSGNCGLYSSGMWFACLSANLNGKYHOKYGRVR-NG:FGNTWFGVSEAHPGGYK 422

Dc 431 DKCIC-KCSQY-TGGWFDAGGPSNLNGMYPQRCTNKFNG:KHYWKG-----SGY- 462

Qy 423 SSFKEAKMMIRPKHF 437

Db 483 -SLKATTMMIRPADF 496

RESULT 5

AAR94605 Human TIE 2 ligand 2 derived from pBluescript KS clone.

XX AAR94605 standard; Protein; 496 AA.

AC AAR94605;

DT 28-CCT-1996 first entry

XX XX VNLMTTMSSTSNAKDPVAKEEQISFRDCAEVFKSGHTNGVLTLPNSTEE-KAYCD 314

KW KW Angiogenesis; neovascularisation; tumour development; wound healing;

KW KW TIE; tyrosine kinase with Ig and EGFR homology domains; vector;

KW KW recombinant; clone; diagnosis; ischaemia; thromboembolic disease;

KW KW atherosclerosis; inflammation; diabetes; ligand bodies; delivery;

XX XX targeting.

OS Homo sapiens.

ABY78906 standard; Protein; 496 AA.

ABY78906;

19-MAY-2000 (first entry)

Human angiopoietin-2 (Ang-2); amino acid sequence.

Human; angiopoietin-2; Ang-2; aminophospholipid; vascularised tumour; unconjugated anti-aminophospholipid antibody; tumour blood vessel market; cancer; treatment; angiogenesis.

Homo sapiens.

KD200002584-A2.

20-JAN-2000.

12-JUL-1999; 99AC-JS15600.

13-JUL-1998; 98US-C322672.

22-DEC-1998; 98US-C110608.

(TEXA) UNIV TEXAS SYSTEM.

Thorpe PE, Ran S;

WPI, 2003-182; 75/16.

NPDB; AAZ222-5.

New composition for killing tumour vascular endothelial cells for treating solid tumours, comprises unconjugated anti-aminophospholipid antibody -

Disclosure; Page 223-224; 226PP; English.

This sequence represents the human angiopoietin-2 (Arg-2) amino acid sequence. Ang-2 is a naturally occurring angiogenesis antagonist; when vascular endothelial growth factor (VEGF) levels are low and generally counteracts the blood vessel maturation and stability mediated by Arg-1. Arg-1 is a naturally occurring angiogenesis agonist, and is a maturation or stabilisation factor, converting immature vessels to mature vessels. Both Ang-1 and Ang-2 are useful in a therapeutic approach to the treatment of vascularised tumours. The invention relates to a composition comprising an anti-aminophospholipid antibody or its antigen binding region. The composition is used to kill tumour vasculature endothelia. Cells. Aminophospholipids are stable and specific markers accessible on the luminal surface of tumour blood vessels. Ang-1 or Arg-2 may be used in the composition of the invention. The composition is used to treat malignant or benign vascularised tumours in animals, especially large tumours.

Sequence 496 AA:

Query Match Score 522; DB 21; Length 496;

Best Local Similarity 27.9%; Fred. No. 5-2e-38;

Matches 139; Conservative 74; Mismatches 159; Irrels 124; Gaps 15;

Y 43 LERSRKCE--EAGECPYQVSPPPL-----TIQ---LPKQFSRIEVFKEYVN 84

b 26 MDSIGSKKQYQYQGGSYTJFPEINDCRSSSPVSNQQRDALEYDDSVRIQVZEN 65

y 85 LKE-----IVNSLKKSCQCKLQD2DNGDEGRN3LLPSTGAEVSDN---- 128

b 86 IMENNTQWLMLKENYQDNMKMENYEQGAVQN-----QTAYMIEITNLNU 134

b 129 -----RVRELESEV-----NKLSELRLRAKEEINHGR---LEKJ 161

b 135 TAEQFRKLTDVAQVLNOTRLEQJLCTSTNLKELQJLCTSEINKLQDCSFLKX 194

y 162 NLV-----NMNNIENYVDISKYANJTF-----V 183

b 195 VLAMEDGHIIQIO-QSI-KEEKDOLCVL-VSKCNSIIEEKQKIVATVNNSYLQKCCDEM 254

Qy 184 VNSLDGKCSKCPSQEIQISRPVQHLYIKDSDYAIGRSSETYRVTPDKNSSEFYVCD 243

Db 255 VNLLTMNSTSNAKDPVAKEQISFRDCAEFPKSGHTINGYLTLPNSTEEIKAIKD 3-4

Qy 244 METMGGGATVLOARLDGSTNFTRWDYKAGFGNLRRREFWLNDKTHLUTSKEMILRD 3C3

Db 215 MEAGGGWNIQIQRREGSDVDFOPTWKEKVGFNPNSGEWLGNEFVSGQTINQORYVLKH 374

Qy 304 IEDENGVELYALYDQFYTAEEFKYRLHYGNTNGTAGDALRFNKHYNHLKPFPTPKDN 363

Db 375 EKDEGENEYASLYEHFYLSEEENYRILIKGTGTAGKISSIOPGND----ESTKDGN 430

Qy 364 DRYPSGNCCOLYYSSGGWWPACLSANLNGKYYHOKYRGVR-NGIFWGTVWGVSEAHPGVVK 422

Db 431 DKCLC-XCSQMLRGCGNWEDACGSNLNGMMPQRQNTNKENG1KWWYNGK----SGY- 482

Cy 423 SSFKEAKHMYIRPQHF 437

Db 483 -SLKATTNMRPADF 496

RESULT :0

AAU77946 standard; Protein: 496 AA.

ID AAU77946 standard; Protein: 496 AA.

XX AAU77944;

AC AAU77944;

DT 02-JUL-2002 (first entry)

XX DE Amino acid sequence for human angiopoietin-2.

XX Human; immunoconjugate; anti-vascular endothelial growth factor antibody; anti-VEGF antibody; monoclonal antibody 2C3 ATCC PTA 1595; VEGF receptor; VEGFR2; KDR/Flik-1; VEGFR1; Flt-1; angiogenesis; macular degeneration; vascular neovascular disease; cancer; vascularised solid tumour; AIDS; metastatic tumour; endothelial cell proliferation; inflammatory disorder; atherosclerosis; diabetic retinopathy; corneal graft rejection; acquired immune deficiency syndrome; infection; restenosis; fungal ulcer; sickle cell anaemia; endometriosis; angiopoietin-2.

XX OS Homo sapiens.

XX AU200179401-A.

XX PD 06-DEC-2001.

XX PF 12-OCT-2001; 2001AU-0079401.

XX PR 28-APR-2000; 2000AU-0048049.

PR 12-OCT-2001; 2001AU-0079401.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX P1 Thorpe PE, Brekken RA;

XX DR AU200179401-A.

XX WPI 2002-281368/33.

DR N-PDB; ABK47116.

XX PT Immunoconjugate compositions for treating cancer by inhibiting angiogenesis and for delivering a diagnostic agent to tumour, comprises anti-vascular endothelial growth factor antibody attached to a biological agent.

XX PT Immunoconjugate (Mab) 2C3 ATCC PTA 1595, and significant inhibition of VEGF binding to the VEGF receptor VEGFR (Flt-1). The compositions

CC The present invention relates to antibody-based compositions comprising an immunoconjugate such as anti-vascular endothelial growth factor (VEGF) antibody (Ab) (or its antigen-binding fragment), attached to a biological agent, where the Ab binds to the same epitope as the monoclonal antibody (Mab) 2C3 ATCC PTA 1595, and significantly inhibits VEGF binding to the VEGF receptor VEGFR (Flt-1). The compositions

CC binding to the VEGF receptor VEGFR (Flt-1) without inhibiting

of the invention are useful in therapy, and diagnosis, for inhibiting angiogenesis in an animal having ocular neovascular disease or macular degeneration, and for delivering a biological agent to a vascularised tumour. The compositions can also be used for treating cancer and subjects at risk of developing, a vascularised solid tumour, a metastatic tumour or metastases from a primary tumour. The composition is useful for specifically inhibiting VEGF-induced endothelial cell proliferation, without significantly inhibiting VEGF-induced macrophage, osteoclast or chondroblast function. The compositions can be used for treating various diseases such as inflammatory disorders, atherosclerosis, diabetic retinopathy, restenosis, acquired immune deficiency syndrome (AIDS), blood borne tumours, corneal graft rejection, Crohn's disease, fungal ulcers, infections, sickle cell anaemia, and endometriosis. The present sequence represents human angiopoietin-2. Angiopoietin-2 may be attached or functionally associated with anti-VEGF antibodies.

Query Match	Score	DB	Length	496;
Best Local Similarity	22.0%	Score 522;	DB 23;	
Pred. No.	27.9%	Pred. No.	5-2-38;	
Matches	138;	Mismatches	159;	Indels 124;
Conservative	74;			Gaps 15;
43	LESRGKCE--EAGECPYQVSILPPL-----TQJ-LPKQFSRTEEVFKEVON	64		
y	: : : : : : : : : : : : : : : :			
c	26 MDSGRKKQQVQRSSCSYTFILLEMDNCRSSSSPPVSNAYORDAPLEYDDSVQLQLQLEN	85		
b	85 LKE-----IYNLSIKKSQCDKLQADDNGDPRGNCLLPLSTGAPGEVDN----	128		
b	86 IMENNTOWLMKLNENYICDNMKKMEVEQCNAYON-----OTAVMIEIGTNELNO	134		
y	129 ----RVERLESEV-----INKLSELKNAKEEINVLHGR--LEKL-61			
b	135 TAEQTRKLTDTCVACLNQTRLEGLLEHSLSTNLKEQJLDOTSEBNKUDKRSFLEKK	194		
b	162 NLV-----NNNNENYYDKSRYANLT-----V-----V-----V-----V	183		
b	195 VLAMEDKHLIQGLOSIKEEKDQLOVLVKSKNSLIEELKKTTATVNNSVQCKQHDLMET	254		
b	184 VNPSDLGKCSKCPSCQEQISRPYQVOLHJYKDCSDYXAGKESSETYVTPDKNSSEFYVCD	243		
b	255 VNNNLTNMSTSNSAKDPTVAKEEIQISFRCAEVFKSIGHTINGYTLYTFRNSTB1KAYED	314		
b	244 MERYGGWTVLJQRLDGSNTNFRTWDQYKAGFGNLREFWIGNXKIHLLTKSRENTILRD	303		
b	315 MEAGGGGNTIIQREDGSVDFQRTWKEYKVGGNSPSEYWLGENEFSQLTNQRYVVKH	374		
b	304 LEDFGNSVELALYDQFYYVANEFLFLKRYLRJHGVNNGTAGDALRNHYHDLKPFITPDKN	363		
b	375 LKCHBNEAYSTLYERFVYSEZENYRFLHKGLTGACKISSIGEND---PSKKGDN	410		
b	364 DRYPSGNCGLYSSGWWFDACLSANLACKYHOKYRGV-NGIFKSTMPGVSEAHPGGYK	422		
b	431 DKCIC-KCSCMTGGWWDAQPSNLNGMMYQORTNKENGKINRKYWKG-----SGY-	482		
b	423 SSFKEAKOMKIRPXFHF 437			
b	483 -SLKATMMIRPADF 496			
	RESULT 11			
D	ABU07855	standard; Protein: 496 AA.		
C	ABU07855;			
X	10-MAY-2003	{first entry}		
E	Human angiopoietin 2 (Ang-2).			
X				

KW	neovascularisation; ischaemia; infarction; tissue graft; transplant;
KW	tie receptor tyrosine kinase; angiopoietin 2; ang-2; human;
KW	Tie-2 receptor tyrosine kinase ligand.
XX	
OS	Homo sapiens.
XX	
	WC2C030C4329-A2.
	PN

XPI; 20C3-210341/20.
DR N-PSDF; ABX12556.
XX
PT Identifying modulators of binding between a Tie receptor tyrosine kinase and an Ephrin ligand, useful for promoting neovascularization, comprises contacting a Tie receptor with an Ephrin in the presence of putative modulator -
PT

CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between the receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant
CC Ephrin-Tie biology, aberrant growth, migration or proliferation of ce
CC that express a Tie receptor or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of human angiopoietin 2 (ang-2), a Tie-2 tyrosine recep
CC kinase ligand.
XX Disclosure, page 100-106, 1998, EPO.

Db * 315 MEAGGGGNTIQQREDEGSVDFQRTMKEYVGFGRNPGSEYWLGEFVSQLTNCQRYVLKIH 374
 Qy 304 LEDEPGVELVALQDQYVANEFLAKRHLHGNNGTAGDALRFRHYNHDLKFPTTPDKD 363
 Db 375 LKDGEGNEA5LYSHFYLISSEELAYRIHLKGLTAGKISS10PGND-- PSTRKGGDN 43 C
 Qy 364 DRYPSGNCGLYSSGKWWFDACLSANLNGKYYHCKYRGVR-NGIFWGSTPGVSEAHFPGGYK 422
 Db 431 DKPIC-KCSQMLTGWWFADCGPSRLNQYPPQRTNFKRGKRYWNG-----Soy- 482
 Qy 423 S3FEKA0MMIRPCHF 437
 Db 483 -S3KATMMIRPACF 496

RESULT 12
 ABP8054 ID ABP8064 standard; Protein: 496 AA.
 XX DT 07-MAR-2003 (first entry)
 XX DE Human angiopoietin-2.
 XX Gene therapy; vector; hepatitis B virus; cardiovascular disease;
 XX human; cardiac; vaso-tropic; antiarrhythmic; antiarteriosclerotic;
 XX CS Homo sapiens.
 XX FN W220287594-A1.
 XX P2 37-NCV-2002.
 XX P2 30-APR-2002; 2002WO-US11644.
 XX PR 30-APR-2001; 2001US-287423P.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Chien KR, Hoshijima M;
 XX WPI; 2003-11184/10.
 XX P1 Novel non-viral vector comprises vesicular membrane with hepatitis B envelope protein with cardiac targeting sequence, and nucleotide sequence for gene therapy useful for treating, e.g., heart failure, arrhythmia and atherosclerosis.
 XX PT Disclosure; Page 38-40; 53pp; English.
 XX PS The present sequence is the protein sequence of human angioipoietin-2. The invention provides a non-viral vesicle vector for the delivery of nucleic acid to various cardiac cell types. The vesicle vector contains the hepatitis B virus envelope protein in which at least part of the liver targetting sequence is deleted and replaced with a specific cardiac cell targetting sequence. For example, to selectively target vascular endothelial cells, peptides including angioipoietin-2 are used. The vesicle vector can be delivered intravenously or intra-arterially rather than by more invasive methods such as direct cardiac injection. It can be used to deliver gene products to replace or enhance expression of proteins for treatment of heart failure, arrhythmia, reperfusion injury, atherosclerosis, to promote angiogenesis, etc. The vesicles are highly stable and can be produced in large quantities, making them ideal for gene therapy.
 XX SC Sequence 496 AA;

Qy 43 LESRKCKE-- EAGECPYQYSLPL-----TQ-LPKQFSRLEEVFKEVQN 84
 Db 26 MDSIGKQYQVQHGCSYTFULLPEMDNCRSSSSSPYNSNAQRDAPLEYDSDVQLQVLEN 85
 Qy 85 LKE----- IVNSLKKSCQDCKLQADDNGDPGRNLPLSTGANGEVGDN--- 128
 Db 86 IMENNTOWLMKCENYIQDNMKMKEV1QVNQAVQN-----QTAVMIEIGNLNQ 134
 Qy 129 -----RVRELESEV-----NKLSSELKNAKEEINVLHGR--I.EKL 161
 Db 135 TAEQTRKLTIDVEAQVLNQTRLEQLEHSLSTNLKQJDOTSEINKMOKDRNSPLEK 194
 Qy 162 NIV-----NMNNIENYVDSKVNLT-----V 183

Db 195 VIADEDKHKIQCQSIIKEEKDQLOQVLYSKQNSI-EELBKVVATATNNSVLQROQHDLMET 254
 Qy 184 VNSLDGKCSKCPSP2EQ1QSPVQHLYKDCSDYYAIGKRSSETTYVTCPOPKSSFEVYCD 243
 Db 255 VNLLTMWTSNSNSAKOPTVAKEEQISFRDAEVFKSGHTENGITYLTFPNSTEEZKAYCD 314
 Qy 244 MBTMGGGWTLCQARLGSTNFRTDDYKAFGNLREFWLGNDK2HLLTKSKEMTLRD 303
 Db 315 MEAGGGGWTIITRREGSDVQRTKEYVKGFGNPGEYHILGNEFVSQLMQRYVULKIH 374
 Qy 304 LEDFNGVLYALYDQFVANEFLKYLHVGNNGTAGDALLRNKHYNHDLKFPTPDKDQ 363
 Db 375 LKQWEGNEA5YSHFPLSSEELNYRHLKJLGTGAKISS10SPND---FSTKDGDN 430
 Qy 364 DRYPSGNCGLYSSGKMFDACLSLANLNGKYYHCKYRGVR- NGIFWGTW2GVSEA;IPGGYK 422
 Db 431 DKCIC-KCSQMLTGWWFADCGPSLNQYPPQRQNTNKGK1KNYWKG----SGY- 482
 Qy 423 SSFKEAKNMIRPKHF 437
 DB 493 -SLKATMMIRPACF 496

RESULT 13
 ABC06771 ID ABC06771 standard; Protein: 572 AA.
 XX AC ABGC06771;
 XX DT 13-FEB-2002 (first entry;
 XX DE Novel human diagnostic protein #6762.
 XX KW Human; Chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.

OS Homo sapiens.
 XX WO200175067-A2.
 XX PD 11-CCT-2001.
 XX PF 30-MAR-2001; 2001WO-JS08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE) HYSEQ INC.
 XX DR Manac RT, Liu C, Tang YI;
 XX DR NP2; 2001-619362/3.
 XX DR N-PSDR; AAS70958.

PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

PT Best Local Similarity 27.9%; Pred. No. 5-2e-38; Matches 138; Conservative 74; Mismatches 159; Index 124; Gaps 15;

XX Claim 20; SEQ ID No 3713C; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and poly peptide (II); sequences (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping; and/or recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (II) is useful in gene therapy techniques to restore normal activity of (III) or to treat disease states involving (III). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (III). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00310-ABG3077 represent novel human diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 572 AA;

Query Match Score 522; DB 22; Length 572;
Best Local Similarity 27.9%; Pred. No. 6.5e-38;
Matches 138; Conservative 74; Xmatches 159; Indels 124; Gaps 15;

Qy 43 LESRGCE---EAGECPYQVSPLPL-----210-LPKQFSRIVEFKEYVN 84
Db 102 MDSIGRKQQYQHGCSYTFELPENDNCRSSSPYVSNAVQRDAPLEYDDSVRQLQVZN 161
Qy 85 LKE-----IVNSLKKSCQDCDKLQADJGDPGRNGLLPSTGAPGVGEN--- 128
Db 162 IENNTQWLYKLENYQDNMKMVEIQCNAVQN-----QTAVNIEGTNLNQ 213
Qy 129 -----RVERESEV-----NQSSELRAKKEENVHLGR---LEKL 161
Db 211 TAEQTRKLTDYEAQVNLNOTTBLQLEHSLSNKLEQKLDQNSFLEKK 27C
Qy 162 NIV-----NMANIENYQSYKVNLT-----V 183
Db 271 VLADEDKHHICLQISLKEKQOQZQVLVKNSK1IEELEKKVTAATNNVSLQKQHDLNET 330
Qy 164 VNSLDGKGSKCKPSQEQIQRPVHQLYKDCSDYYA-GKRSSETTYRTPDKNSSFEVYCD 241
Db 331 VNLLTMNSTNSAKDPTVAKEQISFRDCAEVFKSGHTNGIYTLPNSTTEIKAYCC 390
Qy 244 METPGGGMTVLCARLQDSTNFRTWQDYKAFFGNLREFNQNDKTHLTKSKENILRID 303
Db 391 MEAGGGGTTICQPRREDGSVDFTRKEYKVFGNPGSEYMEVPSCLTNQCVYLKIH 450
Qy 304 LEDENGSEVLTQDFFYVANEFLKYR-HVGNYNTAGDALRFNKYNHDLKFTTPDKDN 363
Db 451 LRDMEGREATSVLEHFPLSSEELNRY-HLKGTGTINGKISSISCPND---FSPKGDN 505
Qy 364 DRYPSGNGLYSSGKMFDACTSANLNGKYYHQLKYGVR-NGIZENGTKWEGYSEAHPGYK 422
Db 507 DRCIC-KCSQWLTGGMFDACPSLNQMYPRONTKNEKIKRYWKG----SCY- 556
Qy 423 SSKPEAKCMIRPKHF 437
Db 559 -SLKATTMMIRPKHF PAFD 572

RESUIC 14
ABG11614

Qy 129 -----RVELESV-----NKSSELRAKKEENVHLGR--LEKL 161
ID ABG11614 Standard; Protein; 1033 AA.

XX AC ABG11614;

Cy 162 NLV-----NMNDIENYVDSKVNLT-----V 183
 Db 732 VLAEDRKHIIQLOSKKEEQDQLQVQIVSKNSNIEJEKIVTAVNNSTLQRQCHELMET 791
 Qy 184 WNSLDGKCSKCPQSOBOIQSPQVQHILYKOCSDYYAIGKSSETYRVTPDQNSSSPEVYCD 243
 Db 792 VNLLTMWTSNSANADPTVAKEQISFRDCAEVRSQHTGINTYLIFPNSTBEIKAYCD 651
 Qy 244 METRGGGTVYLQARLQDGSTNTRPQCYKAGFGRNRREWWGNKTHLTKSDEMILRID 363
 Db 852 MEAGGGWTI TORREGSVDIFCRTKEYKGFGPSGEWLGNEFSQLTNQCRYVLUHK 911
 Qy 304 DEFENDVVELAYAIDCFYVANEFLKVLHVANYNTAGDAIRFKYHNHDLKFETTPDKDN 363
 Db 912 LKDWGSGNEATSLVEFFYLSSEPLNTRIALGLSLGTAGKSSS:SC25KD 967
 Qy 364 DRYPPSGNCGLYYSSGMWFDACLSANLNGKXYHQXKRGVR-NGIFWGTMPGVSFAHPGGYK 422
 Db 968 DKCIC-KCS2NLTGSAWWFDAGCPSNLNGMITYPQRONTNKENGKXWYXKG----SGY- 1319
 Qy 423 SFXEAKRQMRPKHF 437
 Db 1020 -SLXATMMRPAADF 1033

RESULT 15

AAW47528
 ID AAW47528 standard; Protein; 498 AA.

AC AAW47528;
 XX DT 09-SEP-1998 (first entry)

DE Amino acid sequence of chimeric TIE ligand 1NIC2F (chimera 1).
 XX Chimeric TIE ligand 1NIC2F; TIE-2 ligand; neovascularisation;
 KW tumour; human.

XX

OS Homo sapiens.

XX

PN W09805779-A1.

XX

PD 12-FBB-1998.

XX

PP 01-AUG-1997;

XX

25-OCT-1996;

FR 96US-0740223.

XX

22-AUG-1996;

XX

96US-C22899.

PA (REGE-) REGENERON PHARM. INC.

XX

Davis S, Yancopoulou GD;

XX

WPI: 1998-145615/13.

DR N-PSDB; ARI18615.

XX

PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound

PT healing

XX

PS Claim 20; Fig 24; 202pp; English.

XX This is the amino acid sequence of the chimeric TIE ligand 1NIC2F.
 CC used in the method of the invention, involving the production
 CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
 CC and host cells used in the method of the invention are useful for
 CC the recombinant production of the ligands. The ligands, etc. are
 CC useful for blocking blood vessel growth, promoting neovascularisation,
 CC promoting the growth or differentiation of a cell expressing the TIE
 CC receptor, blocking the growth or differentiation of a cell expressing
 CC the TIE receptor and for attenuating or preventing tumour growth in
 CC a human.
 XX Sequence 498 AA;

Query Match Similarity 21.9%; Score 521.5%; DB 19; Length 498;
 Best Local Similarity 32.7%; Pred. No. 5.8e-38; Indels 7%; Gaps 14;
 Matches 131; Conservative 61; Mismatches 138; Delins 7%;
 Qy 61 LPPLTIQLPROSRIE-----EVPKEVNLKEIVNSLKKSQDOKLOADDNGPGRN 1:2
 Db 145 LTDVETQVNQTSRLEIOLLENSLSTYKLEROLLQQTNEILIKE-----KN 191
 Qy 113 GJLPSTGAPGEVGDNVRVLESEVNKLSELKNAKEEINVLHG-----RLER-L 161
 Db 192 SJJ-----BHKZLEM-----GKHKEELDTKEEKENLOGLYVTRGTYLIQELEKQL 237
 Qy 162 KLVNMANTENVYDTSKVANLTFTVNSLDGCKSK-----CPSQCEIOSPVCHLZYKCCSDYY 217
 Db 238 NEATTNN-SV1QKQCOLJMDVHVNLYNLCTKEGVVLKGKGRKKEP-----FRDAEVF 290
 Qy 218 AIGKRSSETYRTPDPKNSSFPEVYCDMETHGGWTVLQARDGSTNFTRTQDYKAGFGN 277
 Db 291 KSHTTTGTYLTUFPNSTE1KAYCMEAGGGWTTIQRREGSVDFCRTMKKEYKVGFGN 350
 Qy 278 LRREFWLGNDK-HLLTTSKEMILRILDEDFNVELVALDQFYVANEFLKYLHVENVYNG 337
 Db 351 PSGEWLNLGFNFQSLINQQRVYVUHLKWDNEAASYLVEDFYLSEELNYPIHLGLTG 410
 Qy 338 TAGDALRENKHYNHDLKAFPTTPDKNDRDYPSGNCGLYSSGMFDACLSANLNGKYYHCK 397
 Db 411 TACKISSISQPGRD-----FSTQGDNPNCIC-KCSOMNLGEWFDAQGPSONLNGMYPGR 465
 Qy 398 YRGVR-NGIFNGTWPGYSEAHPGYKSSEKEAKMIRPKHF 437
 Db 466 QNTNKFNSIKWYWKG-----SGY--SLRA-TMMIRPADF 498
 Search completed: November 5, 2003, 16:45:59
 Job time : 100.359 secs

Db :81 TIVVNSLDGKSKCPSEQIQRSPVQHLYIKDCSDYIAIGKRSSE:TYRTPDPPNSSEV 240
 Qy 241 YCDMETMGGTIVQARLGSTNFRTWODKAGGQNLRREFLNLKHKLTSKEM-L 320
 Db 241 YCDMETMGGTIVQARLGSTNFRTWODKAGGQNLRREFLNLKHKLTSKEM-L 320
 Qy 3C1 RIDLEDENGVELYAJJDQFYVANEFLKYRLHGNNGTAGDALRFTKHYNDLKEPTPD 360
 Db 3C1 RIDLEDENGVELYAJJDQFYVANEFLKYRLHGNNGTAGDALRFTKHYNDLKEPTPD 360
 Qy 361 KNDRYPGSGNCGLYSSGWWFDACLSANLNGKHYOKYRGVNGI:FWGSTWPGVSEAHPGG 420
 Db 361 KNDRYPGSGNCGLYSSGWWFDACLSANLNGKHYOKYRGVNGI:FWGSTWPGVSEAHPGG 420
 Qy 421 YKSSFKEAKOMIRPKFKP 439
 Db 421 YKSSFKEAKOMIRPKFKP 439

RESULT 2
 US-10-C96-255-2
 ; Sequence 2, Application US/10C96-255
 ; Publication No. US20030103972A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Clark, David A.
 ; TITLE OF INVENTION: Methods of Modulating Immune Coagulation:
 ; FILE REFERENCE: 9579-37
 ; CURRENT FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 09/442,143
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn version: 3.1
 ; SEQ ID NO: 4
 ; LENGTH: 432
 ; TYPE: PRF
 ; ORGANISM: Murine fg12
 ; JS-10-C96-255-2

Query Match 77 9%; Score 1853 5; DB 11; Length 432;
 Best Local Similarity 77.7%; Pred. No. 6.7e-10;
 Matches 341; Conservative 42; Mismatches 49; Indexes 7; Gaps 4;
 Qy 1 MKLANWFLSSAVLATYGFVANNETEEIKERAKDVCPUVLESRGKCEAEGRCPYQVS 60
 Db 1 MRPGWMLSSAVLAACR-AVEEHNLTEGLEDEASQAPACPARLEGSCR-BGSQCPQQT 58
 Qy 61 LPPTIOLPKQFSRIEEVKEYONLKEIINSLKSCODCKLQADDHDPGNG--GNG 24
 Db 59 LPPTIOLPKQFSRIEEVKEYONLKEIADSLLKSCODCKLQADDHDPGNG--GNG 24
 Qy 121 APGEVGDNVRRELESEYVNLKSELSEKNAKEEINY-HGRLKEK-NLVNNNNNENYDVKYANL 180
 Db 125 AE-TAEDSSVQELSESQVNKLSEKNAKDQIQLQGRLETHLVNNNNNENYDVKYANL 173
 Qy 181 TPYVNSLDGKSKCPSEQIQRSPVQHLYIKDCSDYIAIGKRSSETYRTDPDKNSSEV 240
 Db 174 TAYVNSLDGKSKCPSEQIQRSPVQHLYIKDCSDYIAIGKRSSETYRTDPDKNSSEV 233
 Qy 241 YCDMETMGGWTIVQARLGSTNFRTWODKAGGQNLRREFLNLKHKLTSKEM-L 300
 Db 234 YCDMETMGGWTIVQARLGSTNFRTWODKAGGQNLRREFLNLKHKLTSKEM-L 293
 Qy 3C1 RIDLEDENGVELYAJJDQFYVANEFLKYRLHGNNGTAGDALRFTKHYNDLKEPTPD 360
 Db 61 LPPTIOLPKQFSRIEEVKEYONLKEIINSLKSCODCKLQADDHDPGNGLL-PSTG 120
 Qy 61 LPPTIOLPKQFSRIEEVKEYONLKEIINSLKSCODCKLQADDHDPGNGLL-PSTG 120
 Db 121 APGEVGDNVRRELESEYVNLKSELSEKNAKEEINYDVKYANL 180
 Db 121 APGEVGDNVRRELESEYVNLKSELSEKNAKEEINYDVKYANL 180
 Qy 181 TIVVNSLDGKSKCPSEQIQRSPVQHLYIKDCSDYIAIGKRSSETYRTDPDKNSSEV 240
 Db 181 TIVVNSLDGKSKCPSEQIQRSPVQHLYIKDCSDYIAIGKRSSETYRTDPDKNSSEV 240
 Qy 241 YCDMETMGGWTIVQARLGSTNFRTWODKAGGQNLRREFLNLKHKLTSKEM-L 300
 Db 241 YCDMETMGGWTIVQARLGSTNFRTWODKAGGQNLRREFLNLKHKLTSKEM-L 300
 Qy 301 RIDLEDENGVELYAJJDQFYVANEFLKYRLHGNNGTAGDALRFTKHYNDLKEPTPD 360
 Db 301 RIDLEDENGVELYAJJDQFYVANEFLKYRLHGNNGTAGDALRFTKHYNDLKEPTPD 360
 Qy 361 KNDRYPGSGNCGLYSSGWWFDACLSANLNGKHYOKYRGVNGI:FWGSTWPGVSEAHPGG 420
 Db 361 KNDRYPGSGNCGLYSSGWWFDACLSANLNGKHYOKYRGVNGI:FWGSTWPGVSEAHPGG 420

RESULT 4
 US-10-C96-255-4
 ; Sequence 4, Application JS/10C96-255
 ; Publication No. US20030103974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Clark, David A.
 ; TITLE OF INVENTION: Methods of Modulating Immune Coagulation:
 ; FILE REFERENCE: 9579-52
 ; CURRENT APPLICATION NUMBER: US/10/096,255

CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Mus musculus

Query Match Score 525; Length 496;
Best Local Similarity 32.9%; Pred. No. 5.4e-39;
Matches 127; Conservative 65; Mismatches 154; Indels 40; Gaps 9;

Qy 61 LPPLTICPKQPSRREEVFKEVNLKKSQDCCLQADNGDPRNGLLPSTG 120
Db :42 LT'DEAVCYLNQTRL----ELQLOHSISTNKLKEQLDTSEINKLNKNSFL---- 191

Qy 121 APGEVDNRVRELESEVNKLUSSEJKNAKEEINVLEGR-----EKLNJNKANIEVY 172
Db 192 :-----EQVKLMEGRHSEELQSMREQDOLQVLVSKQSSVIDELEKRATVATN-SL 243

Best Local Similarity 77.7%; Pred. No. 6.7e-49; Mismatches 7; Indels 7; Gaps 4;
Matches 341; Conservative 42; Mismatches 42;

Qy 1 MKLANYWLSAASUALTYGFELVANNETEEKDRAKDVSPVRLERSRGKCEAEAGCpxQVS 60
Db 1 MRLPEWLWLSAVALAACR-AVEEHLTEGLEDASRQAACPARLEGSGRC-BGQQCPFQLT 58

Qy 61 SPPTCPLPKQFSR-BEVFKEVNDRKNSKSCDKLQADNGDGRNS-LLPSTG 120
Db 59 LPPLTICPKQPSRREEVFKEVNLKKSQDCCLQADNGDGRNS-LLPSTG 114

Qy 121 APGEVDNRVRELESEVNKLUSSEJKNAKEEINV.HGR-EKLNJNKANIEVYDSKYAN 140
Db 115 AB-TEDSRVQELAZQVNKLUSSEJKNAKEEINV.HGR-EKLNJNKANIEVYDSKYAN 173

Qy 181 TFWVNSLDGKCSKCPSQECISCPYCHLIVKDCSDYYAIGKRSSETYRTPDPROSSEN 24C
Db 174 TFWVNSLDGKCSKCPSQEHMQSPQVQHLYIVKDCSDHYVGRSSGAYRTPBHRNSSEV 233

Qy 242 YCDMETMGGKNTVLCARLQGSTNFTWDYKAGGNLREFRGNDKHLLTKSKETL 300
Db 234 YCDMETMGGKNTVLCARLQGSTNFTWDYKAGGNLREFRGNDKHLLTKSKETL 292

Qy 301 RDLDEFDNGVELYALDQFYVANEFLKYRLHGNGNTAGDALRFRNKYHDLKFTFPD 360
Db 294 RIDJEFGLTLIAYJDQFYVANEFLKYRLHGNGNTAGDALRFRNKYHDLKFTFPD 353

Qy 361 KDNDRYPSGNGCGLYSSGNGPACUSANLNGKYYHQYKGVRSNGFTWPGNSEAHCG 423
Db 354 RNDRYSGNGCGLYSSGNGPACUSANLNGKYYHQYKGVRSNGFTWPGNQACCG 413

Qy 421 YKSSPF3AKMTRPKFKP 439
Db 414 YKSSPF3AKMTRPKFKP 432

RESULT 5
US-10-263-677-9
; Sequence 9, Application US/10263677
; Publication No. US2003009994A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Spiegelman, Bruce M.
; APPLICANT: Yoch, Clifford H.
; TITLE OF INVENTION: NOVEL PROTEIN AND NUCLEIC ACID MOLECULES
; FILE REFERENCE: MNI-115CP2
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/546,547
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/261,004
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 09/032,539
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 496

TYPE: PRT
ORGANISM: Mus musculus

Query Match Score 524; Length 496;
Best Local Similarity 32.9%; Pred. No. 6.7e-39;
Matches 127; Conservative 65; Mismatches 154; Indels 40; Gaps 9;

Qy 61 LPPLTICPKQPSRREEVFKEVNLKKSQDCCLQADNGDPRNGLLPSTG 120
Db 142 LT'DEAVCYLNQTRL----ELQLOHSISTNKLKEQLDTSEINKLNKNSFL---- 191

121 AFGEYGDNRVRELESEYNKLSSELXNAKEEINVHLGR-----EKLNJNQNN-ENY 172
 Dc 192 ---- EOKYLCMEEHRSEQLQSMEEQKDILQVLYSKOSVIDEERKLVTAVNN--S; 243
 Dc 173 VDSKVANLTIVNSLDGCKSKCPSSQFQICRPPVQHLYKDCSYAIGKRSETTYTVPD 232
 Dc 244 LQKQHCLMENVSLTUMMESSNSVSSVATRKEEGTFRDCAEFKSLUTTS-S-YTLTFP 303
 Cy 233 PRNSSEVEYCOMETWGGVWVYILOARDGSTSNTRACDYGAGFNLRLREFWLGRDKTHL 292
 Dc 304 NSTEELIKAYEDMDVSGGWTVIQRHEDGSDFQTKEYKEFGPNPLGEYMLGREFSQL 363
 Cy 293 TSKEMILRLCDEDFGVELYAYDGFYVANEFLKYRLHVGNNTAGDALRNKHYNIC 352
 Dc 364 TGCHRVLKIQDVGNEAHSYCHFYLAGEESYRIHTGLTSTAATSS-SQPGE- 422
 Qy 353 LKFETTPDKNDYRPSGNCGLYSSGWNEDACLSANNGRYKHYKRGVR-NGLFNGTWP 411;
 Dc 423 -- -FSTKDSNDKJC-KCSCMLSGMMWFCAGPSN-LNGYYFQONTNKGIRKWWK 478
 Qy 412 GVSSEAHPGGKRSFSRAREOMXPRPF 437
 Dc 479 G-----SGY-SLAKATTXNIRPADF 496

RESULT 7
 US-10-225-060-8
 / Sequence 8, Application US/10225c6
 / Publication No. US20030092891A1
 / GENERAL INFORMATION:
 / APPLICANT: Davis et al.
 / TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
 / FILE REFERENCE: REG 333-2
 / CURRENT APPLICATION NUMBER: US/1C/225,060
 / PRIORITY FILING DATE: 2002-08-21
 / PRIORITY APPLICATION NUMBER: US/09/709,186
 / PRIOR FILING DATE: 2000-11-09
 / PRIOR APPLICATION NUMBER: 08/740,223
 / PRIOR FILING DATE: 1996-10-25
 / NUMBER OF SEQ ID NOS: 30
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 8
 / LENGTH: 480
 / ORGANISM: Homo sapiens
 US-10-225-060-8

Query Match 22.0%; Score 522; DB 15; Length 480;
 Best Local Similarity 27.9%; Pred. No. 9.7e-39; Indels 124; Gaps 15;
 Matches 138; Conservative 74; XMatches 159; Indels 124; Gaps 15;

Query Match 22.0%; Score 522; DB 10; Length 436;
 Best Local Similarity 27.9%; Pred. No. 1e-30; Indels 124; Gaps 15;
 Matches 138; Conservative 74; XMatches 159; Indels 124; Gaps 15;

Query 43 LERSGKCE--EAGECPYQVSILPPL-----TQ---LPKQFSRIEEVEPKEVQN 84
 Dc 26 MNSIGKQYQVQHGSCSYTEFLPEMDNCRASSSSSPYVSNAQORDAPLEYSVCRQVLEN 85

Qy 85 LRE-----IVNSLKRKSCOPDKLOADNGDPEGRNGLLPSTGAGEGEVGN----- 128
 Dc 86 IMENNTQWMLKNEYQDNMKMENYIQQARVCN----- QTAVMIEGTNLLNQ 134

Query Match 22.0%; Score 522; DB 10; Length 436;
 Best Local Similarity 27.9%; Pred. No. 1e-30; Indels 124; Gaps 15;
 Matches 138; Conservative 74; XMatches 159; Indels 124; Gaps 15;

Query 43 LERSGKCE--EAGECPYQVSILPPL-----TQ---LPKQFSRIEEVEPKEVQN 84
 Dc 10 YDSIGKQYQVQHGSCSYTEFLPEMDNCRASSSSSPYVSNAQORDAPLEYSVCRQVLEN 85

Qy 85 LRE-----IVNSLKRKSCOPDKLOADNGDPEGRNGLLPSTGAGEGEVGN----- 128
 Dc 70 IMENNTQWMLKNEYQDNMKMENYIQQARVCN----- QTAVMIEGTNLLNQ 143

Query Match 22.0%; Score 522; DB 15; Length 480;
 Best Local Similarity 27.9%; Pred. No. 1e-39; Indels 124; Gaps 15;

Query 43 LERSGKCE--EAGECPYQVSILPPL-----TQ---LPKQFSRIEEVEPKEVQN 84
 Dc 119 TAEQTRLTDVAVQVNQTTRELQLEHNSLTKLEKOIOLDQEQBINKLQDMSFLEK 178

Qy 162 NV-----MNNTENYQSKVANLT----- 183
 Dc 179 VIAMEDKHHIIQLOSISIKEKDQQLQVLVKQSNSIIELEKK-VTATVNSVLOQHQHDLEYT 236

Qy 184 VNSLDGKCSKCPSCQSQRPVQEYKQDYYAIGKRSETTYTVPDKNSSEFEYVD 243
 Dc 239 VNNJLTMXSTSASAKOPTVAKEQISERDCAEVFKSFTIKA耶D 298

Qy 244 METMGGGWTQIQLDGSNTFRDQYKAGFGNLRREFLGNDKIRLJLTKSKENILRID 333

Dc 293 YEAGGGWTIQCREGSVDFQRTKEYKQFGNPSGEYWLGNENEVSQTNQQRVULK-H 358
 Qy 304 LEDFNGVELYALYDQFYVANEFLKYRLHVNYNGTAGDAEJRFNKHYNHDLKFFTPDKEN 363
 Dc 359 LRDWEGNEAASYEHYLSSLENLRIHLGLT-SAGKISSISQGND----FSTKDGDN 414
 Qy 364 DRYPGNGCGLYSSGGMWFDACJSANLNQKXHCKYRGVR-NG1FNGTWP-GVSEAHPGGYK 422
 Dc 415 DKCIC-KCSCMLTGGMWFCAGPSN-LNGMYPGRONTNKNGIKRYWWK-----SSY 466

Qy 423 SSFKEARMATIPKHF 437
 Dc 467 -SLKATMMIRPADF 480

RESULT 8
 US-C9-998-831-4
 / Sequence 4, Application US/09998831
 / Patent No. US20020119133A1
 / GENERAL INFORMATION:
 / APPLICANT: Philip E. Thorpe
 / APPLICANT: Rolfe A. Brekken
 / TITLE OF INVENTION: ANTI BODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
 / INHIBITING VEGF
 / FILE REFERENCE: 4001_002584
 / CURRENT APPLICATION NUMBER: US/09/998,831
 / CURRENT FILING DATE: 2001-11-30
 / PRIORITY APPLICATION NUMBER: 09/561,108
 / PRIORITY FILING DATE: 2000-04-28
 / NUMBER OF SEQ ID NOS: 44
 / SEQ ID NO: 4
 / LENGTH: 496
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-C9-998-831-4

Query Match 22.0%; Score 522; DB 10; Length 436;
 Best Local Similarity 27.9%; Pred. No. 1e-30; Indels 124; Gaps 15;
 Matches 138; Conservative 74; XMatches 159; Indels 124; Gaps 15;

Query 43 LERSGKCE--EAGECPYQVSILPPL-----TQ---LPKQFSRIEEVEPKEVQN 84
 Dc 85 LRE-----IVNSLKRKSCOPDKLOADNGDPEGRNGLLPSTGAGEGEVGN----- 128
 Dc 86 IMENNTQWMLKNEYQDNMKMENYIQQARVCN----- QTAVMIEGTNLLNQ 134

Query Match 22.0%; Score 522; DB 10; Length 436;
 Best Local Similarity 27.9%; Pred. No. 1e-30; Indels 124; Gaps 15;
 Matches 138; Conservative 74; XMatches 159; Indels 124; Gaps 15;

Query 43 LERSGKCE--EAGECPYQVSILPPL-----TQ---LPKQFSRIEEVEPKEVQN 84
 Dc 135 TAEQTRLTDVAVQVNQTTRELQLEHNSLTKLEKOIOLDQEQBINKLQDMSFLEK 194

Qy 162 NV-----MNNTENYQSKVANLT----- 183
 Dc 195 VIAMEDKHHIIQLOSISIKEKDQQLQVLVKQSNSIIELEKK-VTATVNSVLOQHQHDLEYT 254

Qy 184 VNSLDGKCSKCPSCQSQRPVQEYKQDYYAIGKRSETTYTVPDKNSSEFEYVD 243
 Dc 255 VNNJLTMXSTSASAKOPTVAKEQISERDCAEVFKSFTIKA耶D 314

Qy 244 METMGGGWTQIQLDGSNTFRDQYKAGFGNLRREFLGNDKIRLJLTKSKENILRID 333

Dc 315 YEAGGGWTIQCREGSVDFQRTKEYKQFGNPSGEYWLGNENEVSQTNQQRVULK-H 374

Qy 375 LRDWEGNEAASYEHYLSSLENLRIHLGLT-SAGKISSISQGND----FSTKDGDN 430

Qy 364 DRYPGNGCGLYSSGGMWFDACJSANLNQKXHCKYRGVR-NG1FNGTWP-GVSEAHPGGYK 422

Qy 431 DKCIC-KCSCMLTGGMWFCAGPSN-LNGMYPGRONTNKNGIKRYWWK-----SSY 482

Qy 423 SSFKEAKRMIRPKRF 437
 Db 483 -SLKATMMIRPADF 496

RESULT 9

US-09-897-306-14

Sequence 4, Application US/09938633

Publication No. US2003008218A1

GENERAL INFORMATION:

APPLICANT: THCRE, PHILIP E.
 APPLICANT: RAN, SOPHIA
 TITLE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TO AMINOPHOSPHOLIPIDS
 FILE REFERENCE: 4001_0G2200
 CURRENT APPLICATION NUMBER: US/09-998-833
 CURRENT FILING DATE: 2001-11-30
 PRIOR APPLICATION NUMBER: US/09-351,543
 PRIOR FILING DATE: 1999-07-12
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 4
 LENGTH: 496
 TYPE: PRT
 ORGANISM: Homo sapiens
 JS-09-998-833-4

Query Match 22.0%; Score 522; DB 11; Length 496;

Best Local Similarity 27.9%; Prec. No. 1e-38;

Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

FEATURE: NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. JS20020:23354A1 S2257933

US-09-897-306-14

Query Match 22.0%; Score 522; DB 10; Length 496;

Best Local Similarity 27.9%; Prec. No. 1e-38;

Matches 136; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

Cy 43 LESRGCE--EAGECPYCVSPLPPL-----TIG-LPKQFSRIEEVFKEVQN 84

Db 26 WDSIGKQVQVCHGSCTYTULPMNDNCSSSPVSVNAVRDAPLDDSVRLQLEN 65

Qy 85 LKE-----VNSLKKSCDCKLQADNDPGRNLIPSTARGVCD-----

Db 86 IMENNTQWLNKLENVYQDNRKBNKVEIQCNAVN-----

Qy 86 IMENNTQWLNKLENVYQDNRKBNKVEIQCNAVN-----

Db 87 VVAMIEGTNLLNQ 134

Qy 129 -----RRELEASEV-----

Db 135 TAEGTRKLTVTVEACY-LKTTRELQLEHSLSTKL-EKQIDOTSEIRLQDRNSFLERK 154

Qy 162 KJV-----NMNNIENYVDSKVNANLF-----

Db 195 VVAYEDKHIIQLQS-KEEKQCLQVLVSKNSNIIIELEKIVTAVNSVLCQOHDLMET 254

Qy 196 VNSLDGRCSCKCPSEQQICSPVQHLIYKDCSDYIAIGKRSSETYRVTPDKNSPEYVCD 243

Db 255 VNLLTMMSNSNAKDPVKEEQISFRDAEVFKSGHTINGVYLTFNSTEIKAYCD 314

Qy 244 YETMGGGWTYQARLQGSTNFTRTMDYKGFNRREFWLQNDKHLTKSKEMILRID 323

Db 315 NEAGGGGTWITQRREDGSVFORTKEYKGFGPSGEYWLGNFVSQINQPYVLKH 374

Qy 304 LEDFNGVELYALDQFYVATEFFKYLHVQNYNTAGDLRFNHYHDLKFPTTPDKDN 363

Db 375 LKQWNEANASLYEFYLSSEELAYRIKGLTAGKISSISPGND---FATKOGDN 430

Qy 364 DRYPSGNGLYSSGMWFDSLCSANLNGKYHOKYRGVR-NGIWTGTVGSEAHPGGYK 422

Db 431 DKC1-KC5QMLTGGSWFDACGPNSLNMGYYPQRONTNKPGKWWYNG-----SGY- 482

Qy 423 SSFKEAKRMIRPKHF 437

Db 483 -SLKATMMIRPADF 496

Qy 304 LEDFNGVELYALDQFYVATEFFKYLHVQNYNTAGDLRFNHYHDLKFPTTPDKDN 363

Db 375 LKQWNEANASLYEFYLSSEELAYRIKGLTAGKISSISPGND 430

Qy 364 DRYPSGNGLYSSGMWFDSLCSANLNGKYHOKYRGVR-NGIWTGTVGSEAHPGGYK 422

Db 431 DKC1-KC5QMLTGGSWFDACGPNSLNMGYYPQRONTNKPGKWWYNG-----SGY- 482

Qy 423 SSFKEAKRMIRPKHF 437

Db 483 -SLKATMMIRPADF 496

Sequence 4, Application US/09938633

Publication No. US2003008218A1

GENERAL INFORMATION:

APPLICANT: Chien, Kenneth;

APPLICANT: Hoshijima, Masahiko,

TITLE OF INVENTION: A viral vesicle vector for cardiac specific 3

RESULT 10

US-09-998-833-4

Sequence 13, Application US/10116819

Publication No. US2003166593A1

GENERAL INFORMATION:

APPLICANT: Chien, Kenneth;

APPLICANT: Hoshijima, Masahiko,

TITLE OF INVENTION: No. US2003166593A1-viral vesicle vector for cardiac specific 3

FILE REFERENCE: 6627-PA1198

CURRENT APPLICATION NUMBER: US/10/116,819

CURRENT FILING DATE: 2002-04-10

PRIOR APPLICATION NUMBER: 60/287,423

PRIOR FILING DATE:	2001-04-30
NUMBER OF SEQ ID NOS:	16
SOFTWARE: Patentin version 3.1	
SEQ ID NO: 3	
LENGTH: 496	
TYPE: PRT	
ORGANISM: Homo sapiens	
US 10-136-819-13	
Query Match	22.0%
Best Local Similarity	27.9%
Matches 138 /保守性 7	
QY 43 JESRGKCE --EAEBCPYYV DDB 26 MDSIGKKQKVQCHSSCSCTY	
QY 85 LKE-----IVN QY 96 IMENNTQWIMK-JENYIQQD	
QY 129 -----RVERBLESEY--	
QY 135 TAEQTRKLIDVEAVLNQ	
QY 162 NLV-----	
QY 195 VLAMEDKH-IQLQSIKEEE	
QY 184 VNISTDGKCSRCPSEOBQICE	
QY 255 VRNLLTMMSTSNSAKDPTV	
QY 244 YETMGGGWTVQARLDGSST	
QY 315 MEAGGGGWWTQIRPDRGSY	
QY 304 LEDFNGVETIAYLDPQFYVVA	
QY 375 LKDMEGNEXNSLYBHFYLS	
QY 364 DRYPSGNCGGLYSSGWWMFPE	
QY 431 DKCZC-KCCQMLTGAWNFPE	
QY 423 SSFEEAKMIRPKHE 43	
QY 483 -SLLATMVRPADS 49	
RESULT 12	
US 10-17-615-6	
Sequence 6 Application US/1011	
Publication No. US20130166557A1	
GENERAL INFORMATION:	
APPLICANT: Davis, Samuel, et al.	
TITLE OF INVENTION: TIE-2 LIGA	
FILE REFERENCE: REG 330-C-F.PCT	
CURRENT APPLICATION NUMBER: US	
CURRENT FILING DATE: 2003-06-06	
PRIOR APPLICATION NUMBER: US/	
PRIOR FILING DATE: 1993-09-16	
NUMBER OF SEQ ID NOS: 6	
SOFTWARE: FastSEQ for Windows	
SEQ ID NO: 6	
LENGTH: 496	
TYPE: PRT	
ORGANISM: Artificial Sequence	
FEATURE: Unknown	
OTHER INFORMATION: Unknown C	
US 10-17-615-6	
Query Match	22.0%

RESULT 14
 / Sequence 4, Application US/10373561
 / Publication No. US20031715276A1
 / GENERAL INFORMATION:
 / APPLICANT: Philip E. Thorpe
 / ATTORNEY: Rolf A. Brekke
 / TITLE OF INVENTION: ANTI-BCDY METHODS FOR SELECTIVELY INHIBITING VEGF
 / FILE REFERENCE: 4006_002582
 / CURRENT FILING DATE: 2003-02-24
 / PRIOR APPLICATION NUMBER: US/09/561,439
 / PRIOR FILING DATE: 1999-04-28
 / NUMBER OF SEQ ID NOS: 44
 / SEQ ID NO 4
 / LENGTH: 496
 / SCHEM: Patent in Ver. 2.C
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-10-373-561-4

Query Match 22.0%; Score 522; DB 12; Length 496;
 Best Local Similarity 27.3%; Pred. No. 1e-38;
 Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

Db 108 VNLSJDKCSKCPSEQIQSPVQHLYKDCSDYYAIGKRSSETYRVPDPKNSSEFYVCD 243
 Qy 135 TAETCRKLTDVEAQVLNCTPRLQLEHSLSNKLEQSKDNLQSKNSFLEKK 161
 Db 162 NV-----NMNENYDSKVNLT-----V 183
 Qy 195 VLAMEDKHIIQLOS*KEERDOLQVLVKSKNSIEELKEKIVTATVNNSVLQKQHDLMET 254
 Db 184 VNLDGKCSKCPSEQIQSPVQHLYKDCSDYYAIGKRSSETYRVPDPKNSSEFYVCD 243
 Qy 255 VNLLTMMTSNSAKOPTVAKESQI-----V 183
 Db 255 LDWEGNEAAYSYEHYLSEELNTRIHLGLTPAGKISSQGND---FSTKDGN 430
 Qy 244 METMGCGWTIQLQARLDGSTNFTWDYQKAGFGNLRRREPUGDKIHILTKSKEMLRID 303
 Db 315 MEAGGGWTIQRREGSDVQRTWKEYKVGFGNPGEYMLGNFEVSOLTNQRYVLIK 374
 Qy 304 LEDFNGVELYALYDQFYVANEFLKPLHVGRSYNGTAGDAFLRNHYNHDLKFPTPKDN 363
 Db 375 LDWEGNEAAYSYEHYLSEELNTRIHLGLTPAGKISSQGND---FSTKDGN 430
 Qy 364 DRYPSGNCGLYSSGRNFDAULSANLNGKYHOKYRGVR NGIFPGTWPGVSEAHPGYK 422
 Db 431 DKCIC-KCSQMLTGWMFACGSPNSLNQMGYFQRTONTNKENGKIKWYWWKG---SGV 482
 Qy 304 LEDFNGVELYALYDQFYVANEFLKPLHVGRSYNGTAGDAFLRNHYNHDLKFPTPKDN 363
 Db 375 LDWEGNEAAYSYEHYLSEELNTRIHLGLTPAGKISSQGND---FSTKDGN 430
 Qy 364 DRYPSGNCGLYSSGRNFDAULSANLNGKYHOKYRGVR NGIFPGTWPGVSEAHPGYK 422
 Db 431 DKCIC-KCSQMLTGWMFACGSPNSLNQMGYFQRTONTNKENGKIKWYWWKG---SGV 482
 Qy 423 SSFKEARMMIRPKHF 437
 Db 483 -SLKATTMMIRPADF 496

RESULT 15
 US-10-179-744-6
 / Sequence 6, Application US/10179744
 / Publication No. US2002C17362A1
 / GENERAL INFORMATION:
 / APPLICANT: Davis Samuel et al.
 / TITLE OF INVENTION: T12-2 LIGANDS, METHODS OF MAKING AND USES THEREOF
 / CURRENT APPLICATION NUMBER: US7/0179,744
 / CURRENT FILING DATE: 2002-06-24
 / PRIOR APPLICATION NUMBER: US7/0179,744
 / PRIOR FILING DATE: 1999-09-16
 / NUMBER OF SEQ ID NOS: 6
 / SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO 6
 / LENGTH: 496
 / FEATURES:
 / ORGANISM: Artificial Sequence
 / OTHER INFORMATION: Unknown Organism
 JS-10-179-744-6

Query Match 22.0%; Score 522; DB 14; Length 496;
 Best Local Similarity 27.9%; Pred. No. 1e-38;
 Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

Db 43 LESRGKCE--EAGECPYCYSPLPPL-----TIO--LPKCFSSRIEEVFKEVON 84
 Qy 43 LESRGKCE--EAGECPYCYSPLPPL-----TIO--LPKCFSSRIEEVFKEVON 84
 Db 26 MDSIGRKQYQOHGSCSYTFLLPEMDNCRSSSSPYVSNAVORDAPLEYDDSVQRQCVLEN 85

Qy 85 LXE-----IVNSLJKSCQDKLQADDNGPGRNLPLSTGAPEGVDN----128
 Db 86 IMENNTQMLKLENYCNMKEMVIEQNAVN-----QTAVMIEIGTMNLNQ 134

Qy 129 -----RVRELEASEV-----NMNNTENYDVSKWANLTF-----V 183
 Db 135 TAOTRKLTIDVEAQVLNQTRLEHSLSNKLEQKLDGTSSINLQDKNSFLEKK 194
 Qy 162 NLV-----V 183
 Db 195 VLAMEDKHIIQLOS*KEERDOLQVLVKSKNSIEELKEKIVTATVNNSVLQKQHDLMET 254

Qy 184 VNLDGKCSKCPSEQIQSPVQHLYKDCSDYYAIGKRSSETYRVPDPKNSSEFYVCD 243
 Db 255 VNLLTMMTSNSAKOPTVAKESQI-----V 183
 Qy 244 METMGCGWTIQLQARLDGSTNFTWDYQKAGFGNLRRREPUGDKIHILTKSKEMLRID 303
 Db 315 MEAGGGWTIQRREGSDVQRTWKEYKVGFGNPGEYMLGNFEVSOLTNQRYVLIK 374
 Qy 364 LEDFNGVELYALYDQFYVANEFLKPLHVGRSYNGTAGDAFLRNHYNHDLKFPTPKDN 363

Db 375 LKDWEQEAEASLYEHYLSSSEELNYRIHLKSGJGTAGKISS:SCPGND---FSTKDCDN 430
Qy 364 DRYPSGNGLYSSGWFDALESAEJNGKTYHQKRGVR NSFWGTRHGSVSNHPPGGIK 422
431 DKCIC-KCSQNLTGGSWFDAAGPSNLNGMYPGRONTNKFENGKXAYYNG-----SGY- 452
Db 423 SSFKEARMIRPKHF 437
483 -SLKATTMMTRPAOF 496

Search completed: November 5, 2003, 16:56:14
Cob time : 52.315 secs

GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.

ON protein - protein search, using sw mode:

Run on: November 5, 2003, 16:44:23 ; Search time 30.9427 Seconds
(without alignments)
600.285 Million cell updates/sec

Title: US-09-9C2-563-2
Perfect score: 2378
Sequence: I YKLANWYKLISSAYLATYCFL.....GYKSSPKXAEKDMIRPQSHFKP 425

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 328717 seqs., 42310853 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 3%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:
1: /cgn2_6/pctdata1/iaa/5A-COMB.pep.*
2: /cgn2_6/pctdata1/iaa/5B-COMB.pep.*
3: /cgn2_6/pctdata1/iaa/6A-COMB.pep.*
4: /cgn2_6/pctdata1/iaa/6B-COMB.pep.*
5: /cgn2_6/pctdata1/iaa/PCUTS_COMB.pep.*
6: /cgn2_6/pctdata1/iaa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2378	100.0	439	4	US-09-442-14JA-4	Sequence 2, Appli
2	1853	77.9	432	4	US-09-442-14JA-4	Sequence 4, Appli
3	524	22.0	314	1	US-08-535-50A-2	Sequence 2, Appli
4	524	22.0	436	4	US-09-491-7	Sequence 7, Appli
5	522	22.0	480	3	US-08-700-22A-8	Sequence 8, Appli
6	522	22.0	480	4	US-09-700-18A-8	Sequence 8, Appli
7	522	22.0	436	1	US-08-373-57*-6	Sequence 6, Appli
8	522	22.0	436	2	US-08-418-59*-6	Sequence 6, Appli
9	522	22.0	496	2	US-08-665-92*-6	Sequence 6, Appli
10	522	22.0	436	3	US-09-461-43*-6	Sequence 6, Appli
11	522	22.0	496	3	US-08-700-22A-6	Sequence 6, Appli
12	522	22.0	436	4	US-09-351-457*-4	Sequence 4, Appli
13	522	22.0	496	4	US-09-561-50*-4	Sequence 4, Appli
14	522	22.0	496	4	US-09-561-10*-4	Sequence 4, Appli
15	522	22.0	496	4	US-09-351-541-4	Sequence 4, Appli
16	522	22.0	496	4	US-09-561-52*-4	Sequence 4, Appli
17	522	22.0	496	4	US-09-202-49*-8	Sequence 8, Appli
18	522	22.0	496	4	US-08-817-318*-6	Sequence 6, Appli
19	522	22.0	496	4	US-09-700-18A-6	Sequence 6, Appli
20	522	22.0	496	4	US-09-561-499*-4	Sequence 4, Appli
21	521.5	21.9	498	3	US-08-740-22A-20	Sequence 20, Appli
22	521.5	21.9	498	4	US-09-700-18A-20	Sequence 24, Appli
23	517.5	21.8	499	3	US-08-700-22A-24	Sequence 24, Appli
24	517.5	21.8	499	4	US-09-700-18A-24	Sequence 24, Appli
25	510	21.4	496	3	US-09-740-22A-15	Sequence 15, Appli
26	510	21.4	496	4	US-09-700-18A-15	Sequence 15, Appli
27	506.5	21.3	286	3	US-08-960-5C7-2C	Sequence 20, Appli

ALIGNMENTS

RESULT 4: US-09-442-14JA-2						
Sequence 2, Application US/09442143A						
Patent No. 6403089						
GENERAL INFORMATION:						
APPLICANT: Levy, Gary Clark, David A.						
TITLE OF INVENTION: Methods of Modulating Immune Coagulation						
FILE REFERENCE: 957-14						
CURRENT FILING DATE: 1999-11-15						
PRIOR APPLICATION NUMBER: US 60/046,537						
PRIOR FILING DATE: 1997-05-17						
PATENT APPLICATION NUMBER: US 60/261,684						
PRIOR FILING DATE: 1997-10-12						
NUMBER OF SEQ ID NOS: 53						
SEQ ID NO: 2						
LENGTH: 439						
TYPE: PCT						
ORGANISM: Homo sapiens fg-2						
US-09-442-14JA-2						

Query Matc: 100.0% Score: 100.0% Pred. No.: 8e-211; Best Local Similarity: 100.0%; Matches: 439; Conservative C: Mismatches: 0; Indels: 0; Gaps: 0;						
1 MKLANWYKLISSAVYLAVTATYGFLLVANNETEEIKDERAKDVKPYRLESRGKCEAGECPYQVS 60						
2 Y V T V V N S L D Q K C S R K P S O E Q I Q S R P V Q H L Y K D C S D Y A I G R K S S E T Y R V T P D K N S S F E V 240						
3 1 MKLANWYKLISSAVYLAVTATYGFLLVANNETEEIKDERAKDVKPYRLESRGKCEAGECPYQVS 60						
4 1 L P P T I O L P K Q S R I E E V E K Y O N L K E I V N S L K S C D C K L Q A D D N G D P G R G N G L I P S T G 120						
5 D b 1 L P P T I O L P K Q S R I E E V E K Y O N L K E I V N S L K S C D C K L Q A D D N G D P G R G N G L I P S T G 120						
6 Q y 1 L P P T I O L P K Q S R I E E V E K Y O N L K E I V N S L K S C D C K L Q A D D N G D P G R G N G L I P S T G 120						
7 D b 1 L P P T I O L P K Q S R I E E V E K Y O N L K E I V N S L K S C D C K L Q A D D N G D P G R G N G L I P S T G 120						
8 Q y 1 T F V V N S L D Q K C S R K P S Q E Q I Q S R P V Q H L Y K D C S D Y A I G R K S S E T Y R V T P D K N S S F E V 240						
9 D b 1 T F V V N S L D Q K C S R K P S Q E Q I Q S R P V Q H L Y K D C S D Y A I G R K S S E T Y R V T P D K N S S F E V 240						
10 C y 1 Y C D M E T M G G G W T V Q A R L D G S T M F T R T W Q D Y K A F G F N G L I P S T G 120						
11 D b 1 Y C D M E T M G G G W T V Q A R L D G S T M F T R T W Q D Y K A F G F N G L I P S T G 120						
12 Q y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
13 D b 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
14 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
15 D b 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
16 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
17 D b 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
18 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
19 D b 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
20 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
21 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
22 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
23 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
24 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
25 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
26 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						
27 C y 1 A P G E V G D N V R E L E S E Y N K L S S E L K N A K E E I N Y V D S K Y A N L 180						

RESULT 2

US-09-442-143A-4

Sequence 4, Application US/C9442143A

Patent No. 6431089

GENERAL INFORMATION:

APPLICANT: Levy, Gary

CLARK, David A.

TITLE OF INVENTION: Methods of Modulating Immune Coagulation

FILE REFERENCE: 9519-14

CURRENT APPLICATION NUMBER: US/63/442,143A

PRIOR APPLICATION NUMBER: 1997-11-15

PRIOR FILING DATE: 1997-05-17

PRIOR APPLICATION NUMBER: US 60/146,537

PRIOR FILING DATE: 1997-10-10

PRIOR APPLICATION NUMBER: US 60/061,684

PRIOR FILING DATE: 1997-10-10

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 432

TYPE: PRT

ORGANISM: Murine fg2

US-09-442-143A-4

Query Match 77.9%; Score 1853.5; DB 4; Length 432;

Best Local Similarity 77.7%; Pred. No. 1-7e-12;

Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;

Qy 1 MKLANNWMLSSAVLATYGFVANNETRPEKLEKLNGLVMMNTENVDSVANL 60

Ds 1 MRIGWMLSSAVLAACR-AVEFHNLTEGLDEASADACPALEGSRCA-EQSQQCPFQLT 59

Qy 61 LPPLTICPKQFSRVEEYFKEYQNLLKEIWNSLKKSCDCKLQADJNDGDPGRNGLJLPSTG 120

Ds 59 LPTLTIQPROGSMEEYLKEYVTLKEAVDS-LKKSCDCKLQADJNDGDPGRNGL---GMG 114

Qy 121 APGEVGDNVRVPELESENKLSELSEKNAKEEINVLHGRLEKLNGLVMMNTENVDSVANL 160

Ds 115 AE-TAEDSRVCELESQVNKLSELSEKNAKEEINVLHGRLEKLNGLVMMNTENVDSVANL 173

Qy 181 TTYVNSLDGKCSKPSQBG1QSRREVQHLYDKGSDSYA:KRESSETYRVTPOPNESSFEV 240

Ds 174 TTYVNSLDGKCSKPSQBG1QSRREVQHLYDKGSDSYA:KRESSETYRVTPOPNESSFEV 233

Qy 241 YCDMETYGGWTVIQLARLGSTNFTRTWDYKAGFGNLRREFWLGNDXHILTKSKEMIL 300

Ds 234 YCDMETYGGWTVIQLARLGSTNFTRTWDYKAGFGNLRREFWLGNDXHILTKSKEMIL 293

Qy 301 RIDLEDFNGVELAZYDQFYVANEFLKRLHNMNGTAGDLRENGYHJELKEFTPD 360

Ds 294 RIDLEDFNGVELAZYDQFYVANEFLKRLHNMNGTAGDLRENGYHJELKEFTPD 353

Qy 361 KNDRYPSENCGCLYSSGMFDACCSANINGKYHOKYRGWNG:FACTWPVSEAHPGG 420

Ds 354 RDNDRYPSENCGCLYSSGMFDSCSLSANINGKYHOKYRGWNG:FACTWPVSEAHPGG 413

Qy 421 YKSSFKAKMIRPKHFKP 439

Ds 414 YKSSFKAKMIRPKHFKP 432

Patent No. 586777.1

GENERAL INFORMATION:

APPLICANT: HARA, HIROSHI

YOSHIMURA, HIROMITSU

APPLICANT: MATSUZI, YUMIKO

APPLICANT: SHINDO, SAKU

APPLICANT: HANADA, KAZUNORI

TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1255 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.3.C

CURRENT APPLICATION DATA:

APPLICATION NUMBER: JS/08/525,505A

FILING DATE: 22-SEP-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/00455

FILING DATE: 22-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP C5-063905

FILING DATE: 23-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 314 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08/525,505A-2

Query Match 22.0%; Score 524; DB 1; Length 314;

Best Local Similarity 37.6%; Pred. No. 3.9e-40;

Matches 124; Conservative 46; Mismatches 104; Indels 56; Gaps 13;

Qy 125 VGD-NRVE--LESEVNKLSELSEKNAKEE-I-NVUHGRLEKLNGLVMMNTENVDSVANL 179

Ds 23 LGDENCLQEVRLRAQVROLETRYRQOOVIAQLHEK-EVQFLDRQEDSFID---- 75

Qy 180 LTFVNSLDGKCSKPSQEG1QSRREVQHLYDKGSDSYA:KRESSETYRVTPOPNESSFEV 239

Ds 76 -----LGK-----RH-YADSEIYNDGFKHSGFVKIKPLQSLAEFS 111

Qy 240 YCDMETYGGWTVIQLARLGSTNFTRTWDYKAGFGNLRREFWLGNDXHILTKSKEMIL 296

Ds 112 YCDMSD-GGWTVIQRSDSEENRGRNDYENGFGNNVQSNEYW-JGNNKNLNUZTQG 170

Qy 297 EM1R1D1EFDNGVELAZYDQFYVANEFLKRLHNMNGTAGDLRENGYHJELKEFTPD - - -YN 350

Ds 171 DYTLDKIDCFKNSRFQAYKFKVGDKEFSTGDSLSCTFHPPEVQWMAA 230

Qy 351 HDLKKEFTEDCNDRYPSENCGCLYSSGMFDACCSANINGKYHOKYRG-WRNZPFGT 429

Ds 231 HTQMKFSTRDNDY-NGNAEAEQSGWFRCHSANLNGYYQGPYRATDENGUVWXT 289

Qy 416 WPGVSEAHPGCYKSSFKAKMIRPKHFKP 439

RESULT 3

US-08/525,505A-2

Sequence 2, Application US/08525505A

Db 290 W-----RGWYSLKSVKKIRPSDFP 311

STREET: 777 Old Saw Mill Road

CITY: Tarrytown

STATE: NY

COUNTRY: USA

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/740,223A

FILING DATE: 25-OCT-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/022/939

FILING DATE: 02-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Cobert, Robert J

REGISTRATION NUMBER: 36,108

REFERENCE/DOCKET NUMBER: REG 333

TELECOMMUNICATION INFORMATION:

TELEPHONE: 914-345-7400

TELEFAX: 914-345-7721

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 480 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE: Nature TI2 protein

NAME/KEY: Nature TI2

LOCATION: 1...480

OTHER INFORMATION:

US-CB-740-223A-8

Query Match Score 522; DB 3; Length 480;
Best Local Similarity 27.9%; Pred. No. 1..1e-39; Indels 124; Gaps 15;
Matches 139; Conservative 74; Mismatches 15;

Query 43 LERSRKCE--ERGECPVYVSLPL--.....TIQ-LPKQPSRIEEVFKEYON 84

Db 10 MDSICKKKQVQHGSCTSYFLPZPMDCRSSSSPYVSNAVCRDAPLEYDDSVRQLVLEN 69

Qy 85 LKE-----IVNSLKKSCQDKQIQAQDNGDPGRNGLLPISTGPGEVGDN----28

Db 70 IMENNTQKLMKLENYICOMMKVNEVQQNAVQN-----QTAVMIEGTGNLLNQ 118

Qy 129 -----RVELEY-----NKLSSSEUKNAKEXEETNLHLGR--LLENL 161

Db 192 -----EKVQDYEKGKSEQLMKKEQNDLVLVSKQSSTIDELRKLVATAVRN--SD 243

Qy 173 VDSKVANLTENVNSLQGCKSKPSQEIQSRVQHLYIKQCSDDYIAIGRSSETYRPTD 232

Db 244 LQKCOHLMETNSLTMSSPNKSSVAIREKEOCTPROCAEIKPSGLTSGIVLTTFP 303

Qy 233 PNSSSFEVYCDMETGGWTWQDARLQGSTTRTKDQYKAFGNNPREFJGNDKTHL 292

Db 304 KSTEETIAYCDVGGGWTWQHREDSVDFORTKEYKEFGNPGLGEYMGNEVSQL 363

Qy 293 TKSKEMLRDLDEDFGVELYALDOFYVANEFLKYR-LHVGRNYNTAGDALRFNKHYHD 352

Db 364 TGHRYVWKIQJDWEGNEAHSSYDHFLAGESNVYIHLTG-LTGAKISSISQGSD- 422

Qy 353 LKFFTTPDKDNDRYPSSNCGLYSSGWNEDACLSANINGKHYQKRYGR-NGIPNGTWP 411

Db 423 -- FSTKCSDNKRCZC-XCSQNLSSGWNEDAGPSNINLGYCFCKRTQNKENGKHYWK 478

Qy 412 GYSEAHPGQYKSSFEKAKMTRPKHF 437

Db 479 G-----SGY-SUKATTMMIREADF 496

Qy 8044 METRGGGTVLQARDGSIITRTWQYAGFGNLREWLGNDKIHLLTKSKEMLRBD 303

Db 299 MEAGGGWWTQREDGSDUTQRTWKEYKVGFPNSGEWLGNEFVUSLNTQRYVLUKTH 358

Qy 304 LEDFNGVLYALDOFYVANEFLKYR-LHVGRNYNTAGDALRFNKHYHDLKFTTPDKDN 363

Db 359 LKDWEQEASLYHFYLSEELUNYRHLKGLTGAGKISSISQPGND---ESTKDSDN 414

Qy 364 DRYPGNCGLYSSGWNEDACLSANINGKHYQKRYGR-NGIPNGWPGVSAHPGSKY 422

Db 415 DKCIC-KCSQMLTCGWWFACGSNLNGHYPQRGNTNKFNGKMYWKG----SCY- 466

RESULT 5
US-08-740-223A-8
Sequence 8, Application US/08740223A
Patent No. 626564
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signaling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.

Qy 423 SFPEAKKMRPKEPF 437
 Db 467 -SLKATMMIRPADF 480

RESULT 6
 JS-09-709-188-8
 Sequence 8, Application US/09709188
 ; Patent No. 6441237
 ; GENERAL INFORMATION:
 ; APPLICANT: DAVIS et al.
 ; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
 ; FILE REFERENCE: REG 333-2
 ; CURRENT APPLICATION NUMBER: US/09709,188
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: 06/744,223
 ; PRIOR FILING DATE: 1996-10-25
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 8
 ; LENGTH: 48C
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-709-188-8

Query Match Score 22.0%; Best Local Similarity 27.9%; Matches 138; Conservative 74; Mismatches 159; Indels 24; Gaps 15;
 Best Local Similarity 27.9%; Pred. No. 1.e-39; Indels 24; Gaps 15;

Qy 43 LESRKCE---EAECPYQVSPPL----
 Db 10 MDSIGKKQYQVOHGSCTFLPEMENCRSSSPYVNAVORDAPLEYDSTWRLQVLEN 6 9
 Qy 85 LKE-----IVASLKRSCQQCKLQADDNGDPRGRNLULPSGAPGVGDN----
 Db 76 IWMNTQWLMKLENYIQDNMKEMVEIQNAVAN-----QTAVMIEGTNLLNQ 118
 Qy 129 -----RVERESEY-----
 Db 119 TAETQRKLTDVEAQVLNQTRLEQILEHSLSTNKLQEQDTEINKLQDNNSFLEKK 178
 Qy 162 NIV-----
 Db 179 VLAEDCKHIIQLQSIKEEXDCLQVLVKSONSKITELELKIVTAVNNVSVLQKQHDLME? 238
 Qy 184 VNSLDGKCSKCPSEQIQRPVQHLYKDCSYAIGRSSETTYRTPDKPSSFEYVCD 243
 Db 239 VNNLJTMSTSNSAKDPTVAKEEQISERDKCAEVFKS3HTINGYUZFPNSTEEIKYCD 299
 Qy 244 METNGGGMTVQLQARLDGSTNFTRWQDYKAGFGNLRRREFNLGNDKIH-LTKSKEMI-RID 303
 Db 299 MEAGGGWITLQQRDEGSDFORTWKEFVGFGNPGEYNLNGEFVSLTRQYVKEKH 358
 Qy 304 LEDFNGVELAYDQFYVANEFLKYRHVNNGNTAGDALRPNKHYNHCLXPKTTIPKDN 363
 Db 359 LKQWEGREASLYBHFLUSELNVRYHLKGZTAGKISSSQPGND---FSTXGSDN 414
 Qy 364 DRYSGNCMLGYYSSGWWFACLSANLNGKYYKSYRGVR-NIGIFWGMWPGVSEAHPG3YK 422
 Db 415 DKCIC-KC5QMLTGGWWFDAGPSNLNGYYQPQNTKFNFGTKNYWKG----SGY- 466
 Qy 423 SFPEAKKMRPKEPF 437
 Db 467 -SLKATMMIRPADF 480

Query Match Score 22.0%; Best Local Similarity 27.9%; Pred. No. 1.e-39; Indels 124; Gaps 5;
 Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 5;

Qy 43 LESRKCE--EAECPYQVSPPL-----
 Db 26 MDSIGKKQYQVHQHGSCTFLPEMENCRSSSPYVNAVORDAPLEYDSTWRLQVLEN 85
 Qy 65 LKE-----
 Db 86 IMENNTQWLMKLENYIQDNMKEMVEIQNAVAN-----QTAMIEGTNLLNQ 134
 Qy 129 -----RVERESEY-----
 Db 135 TAETQRKLTDVEAQVLNQTRLEQILEHSLSTNKLQEQDTEINKLQDNNSFLEKK 194
 Qy 162 NIV-----
 Db 195 VLAMEDKHIIQLQSIKEEXDCLQVLVKSONSKITELELKIVTAVNNVSVLQKQHDLME? 254
 Qy 184 VNSLDGKCSKCPSEQIQRPVQHLYKDCSYAIGRSSETTYRTPDKPSSFEYVCD 243
 Db 255 VNNLJTMSTSNSAKDPTVAKEEQISERDKCAEVFKS3HTINGYUZFPNSTEEIKYCD 314
 Qy 244 NETMGCGWTVLQQRDEGSDFORTWKEFVGFGNPGEYNLNGEFVSLTRQYVKEKH 161
 Db 315 MEAGGGWITLQQRDEGSDFORTWKEFVGFGNPGEYNLNGEFVSLTRQYVKEKH 374

RESULT 7
 Sequence 6, Application US/08373579
 ; Patent No. 5654340
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, et al.
 ; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES

26 YDSSGKRGQVQHGSCTYFLPEMDNCRSSSPYVSNAQRDAPLEYDDSVGRQVLEN 85
 Db 85 LKE-----IVNSLZEKSCDCCKLOADINGDEGRNGLLPSTGAPGEVGDN---- 128
 Qy :
 Db 96 IMENNTOWMLKGLENYIQQNMKEMVEQQNAVN-----QTAVMEGTNLNQ 134
 129 -----RVREJSESV-----NKLSSELXNAKEEINVHLGR--LEKL 161
 Qy :
 Db 135 TABOTRKLTDVEAQVLNCTRLQLEHSLSNLUERQILQTSSEINKLODNSFUEKK 194
 Db 162 NLV-----NMANNENYVDSKVNLT-----V 183
 Qy :
 Db 195 VLAMEDKHIIOLQSIKEKDQLQVLVSKQNNTIELEKKIVTATVNNSVLQKQCHDLMET 254
 Qy :
 Db 194 VNSLDGKESKCPQEIQSQRPVQHLIKYDCAKCSDYAIGRSSESTYRTPDPKNSSEFVYCD 243
 :
 Db 255 VNNLTYMNTSTSNAKDPTVAKEEQISPRDCAEVKSHTTINGIYTLPNSTEETRAYCD 314
 Qy :
 Db 244 METMGGGGNTVQLARLDGSTNFTRTMQZYKAGFGNLRREFWLQNDKIRHLTTSKEMILRID 3C3
 :
 Db 315 MEAGGGGNTIQREDGSVDFORTKEYVGFNPSEGYWLNEFVSQLTHQCRVYUJZH 374
 Qy :
 Db 304 LEFGNGVELYAYDQFYVANEFLKYLHVGVNGTAGDALRFNKHYNHDKEFTTPDKDN 363
 :
 Db 375 LKWDWGNBAYSLEHFVYLSSEENYRTHKGITGTAKISSISQGRND---FSTKDGDN 430
 Qy :
 Db 364 DRYPSGNGLYWSSEWFDACUSANLNQSKYHQKYRGVR-NCLFWGTWPQYSEAHPGYK 422
 :
 Db 431 DKJC-C-KSOML-TGWNEDACGPSSLNGWYYFORONTNKFCNWKLYWKG----SGY- 482
 Qy :
 Db 423 SSFREAKCMIRPKHF 437
 Qy :
 Db 483 -SLKATTM:MRPADF 496

RESULT: 9
 US-A-665-926-6
 Sequence 6, Application US/08665926
 Patient No. 595197
 GENERAL INFORMATION:
 APPLICANT: Valenzuela et al.
 TITLE OF INVENTION: THE LIGAND-3, METHODS OF MAKING AND USES
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill River Road
 CITY: Tarrytown
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10591-6707
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,926
 FILING DATE: 19-JUN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Robert J. Cobert
 REGISTRATION NUMBER: 35,108
 REFERENCE/DOCKET NUMBER: REG 330-H
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 345-7400
 TELEFAX: (914) 345-2113
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 POLYMER TYPE: linear

US-09-665-926-6

Query Match: 22.0%; Score: 522; DB: 2; Length: 496;
Best Local Similarity: 27.9%; Pred. No. 1.e-39;
Matches 138; Conservatve 74; Mismatches 159; Index: 24; Gaps: 15;

Qy 43 JESRGKGE---BAGECQYCVS:PPPL-----TQ---UFQFSSIEVFKEVN 94
Db 26 MESTGRKQYQVHGSSEYTFLEMDCRSSESSPVNSNAICRDLPEWVORLQVLEN 95
Cy 85 LKE-----TNSLURSKCDOCKLFLGDNPGPGRNLLPSTGAEGVGEN---- 128
Db 86 IMENNTWLMKXENYIODRKXEMEVICQNACM-----QAVXNEIGINLN 134
Qy 129 -----RVREJSEV-----NKSELQXAKKEEINLUGR---LEKL 15;
Db 135 TAEOTTRKLTDVAQVLNOTPLEQLEHSLSNKLEKCLECTSEINKLQDANSFLERK 194
Qy 162 NV-----NMNNENYUSKVALTF-----V 193
Db 195 VLAEDKHIIQJOSIKERKDQQLVLSKQNSLIEELKIVATYNSVLUOKQHDLMET 254
Cy 184 VNSLDGKCSKPSKCPSCQIOSSRPTFHLYKDCSDYYAIGKPSSSETTYKTPDKSSPEVYCD 243
Db 255 VNLLTMMSNTSNSAKDPTVAKEQISERDCAEVFKSHTINGZYLT;FPNSTEEKAYCD 314
Qy 244 NETMGGGWTWJZARLDSSTNFRTRQDYKAEGQNLREFNLNDKHLUTKSKENLIRD 303
Db 315 MEAGGGWTWJTIQRDGSVDORTWKEYKVFGNPSCGEWM-GNEPVSCLTNQRTYLIKH 374
Qy 304 LEDENGVELYALYDQFVIANELKYLHVGNNGTAGDALRNGYANHDLKFTTPDKDN 363
Db 375 LDWEGNEBASUYEHFLISSEELNVTTHLGKTTGAKISSGPOND---FSTKGDN 430
Qy 364 DRYEONGGJYSSGAWNFDACILSANLNGKHYHQVKGVR-NQFENGTWPGYSEAHPGGYK 422
Db 431 DRCIC-KQSOMLITGGWNFDACOPSNLNGMYFQRQNTNKFNG-KWVYWKG----SGY- 482
Qy 423 SSFKEAKOMIRPKHF 437
Db 483 -SLKATTMIMRPADE 496

RESULT 10
US-09-162-437-6
Sequence 6, Application: US/09162437
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/162,437
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C8-418,595
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-09-740-223A-6
Sequence 6, Application US/08740223A
Patent No. 6265564
GENERAL INFORMATION:

RESEQ: 11
US-09-740-223A-6

REGISTRATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
ATTORNEY/AGENT INFORMATION:
NAME: Colvert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-162-437-6

Query Match 22.0%; Score 522; DB 3; Length 496;
Best Local Similarity 27.9%; Pred. No. 1.e-39;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

Qy 43 LESRGKCE---BAGECQYCVS:PPPL-----TQ---UFQFSSIEVFKEVN 84
Db 26 MESTGRKQYQVHGSSEYTFLEMDCRSSESSPVNSNAICRDLPEWVORLQVLEN 85
Qy 85 LKE-----TNSLURSKCDOCKLFLGDNPGPGRNLLPSTGAEGVGEN---- 128
Db 86 IMENNTWLMKXENYIODRKXEMEVICQNACM-----QAVXNEIGINLN 134
Qy 129 -----RVREJSEV-----NKSELQXAKKEEINLUGR---LEKL 15;
Db 135 TAEOTTRKLTDVAQVLNOTPLEQLEHSLSNKLEKCLECTSEINKLQDANSFLERK 194
Qy 162 NV-----NMNNENYUSKVALTF-----V 193
Db 195 VLAEDKHIIQJOSIKERKDQQLVLSKQNSLIEELKIVATYNSVLUOKQHDLMET 254
Db 26 MESTGRKQYQVHGSSEYTFLEMDCRSSESSPVNSNAICRDLPEWVORLQVLEN 85
Qy 85 LKE-----TNSLURSKCDOCKLFLGDNPGPGRNLLPSTGAEGVGEN---- 128
Db 86 IMENNTWLMKXENYIODRKXEMEVICQNACM-----QAVXNEIGINLN 134
Qy 129 -----RVREJSEV-----NKSELQXAKKEEINLUGR---LEKL 151
Db 135 TAEOTTRKLTDVAQVLNOTPLEQLEHSLSNKLEKCLECTSEINKLQDANSFLERK 194
Qy 162 NV-----NMNNENYUSKVALTF-----V 193
Db 195 VLAEDKHIIQJOSIKERKDQQLVLSKQNSLIEELKIVATYNSVLUOKQHDLMET 254
Qy 184 VNSLDGKCSKPSKCPSCQIOSSRPTFHLYKDCSDYYAIGKPSSSETTYKTPDKSSPEVYCD 243
Db 255 VNLLTMMSNTSNSAKDPTVAKEQISERDCAEVFKSHTINGZYLT;FPNSTEEKAYCD 314
Qy 244 METNGGWTVLQFLDQGPNLRLRFLGNDKIHLLTKSEMIIRD 303
Db 315 MEAGGGWTWJTIQRDGSVDORTWKEYKVFGNPSCGEWM-GNEPVSCLTNQRTYLIKH 374
Qy 334 LEQENGVELYALDQFVIANELKYLHVGNNGTAGDALRNGYANHDLKFTTPDKDN 363
Db 375 LKQEGNEASLYHEFLSSEEELNVTTHLGKTTGAKISSGPOND---FSTKGDN 430
Qy 364 DRYEONGGJYSSGAWNFDACILSANLNGKHYHQVKGVR-NQFENGTWPGYSEAHPGGYK 422
Db 431 DKCFC-KCQMLTIGWWFACGPSNLNGMYPORQNTNKFNG-KWVYWKG----SGY- 482
Qy 423 SSFKEAKOMIRPKHF 437
Db 483 -SLKATTMIMRPADE 496

APPLICANT: Davis, et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
 STREET: Regeneron Pharmaceuticals, Inc.
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/740,223A

FILING DATE: 25-OCT-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/N 60/022/999

FILING/AGENT INFORMATION:

NAME: Cober, Robert J.

REGISTRATION NUMBER: 36,105

REFERENCE/COCKETT NUMBER: FEG 333

TELECOMMUNICATION INFORMATION:

TELEPHONE: 914-345-7721

TELEFAX: 914-345-7721

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECUL TYPE: protein

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: Human TIE-2 ligand 2

LOCATION: 1..496

OTHER INFORMATION: from clone pBluescript KS

OTHER INFORMATION: encoding human Tie 2 ligand 2

US-08-740,223A-6

RESULT :2
 US-09-351-457-4
 Sequence 4, Application US/09351457
 Patent No. 6311694
 GENERAL INFORMATION:
 APPLICANT: THORPE, PHILIP E.
 APPLICANT: RAN, SOPHIA
 TITLE OF INVENTION: CANCER TREATMENT METHODS USING THERAPEUTIC CONJUGATES
 THAT BIND TO AMINOPHOSPHOLIPIDS
 FILE REFERENCE: 4001-062300
 CURRENT APPLICATION NUMBER: US/09/351-457
 CURRENT FILING DATE: 1999-07-12
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 4
 LENGTH: 496
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-09-351-457-4

Query Match 22.0% Score 522; DB 4; Length: 496;
 Best Local Similarity 27.9%; Pred. No. 1, 2e-39;
 Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

Query 43 LESRGKCE---EAGECPYQVSPLPP-----TIQ--LPKGFSR1EEVFKEVQN 84
 Db 26 MDSIGKKQQVQHGSCSTFLIPEMDNCRSSSPYVNAQDAPLEYDSDYQRLOVLEN 85

Query 85 LKE-----IVNSLKKSCQCCKLQADNGDB3RNLILLPSTGAPGEVGDN -- 128
 Db 86 IMENNTOWLMKLENYIQQNMKKMVEQQNAYQN-----QAVMISIGTLLNC 134

Query 129 -----RVRELESEV-----NKLSSELKNAKEEINVHLGR--JEKL 161
 Db 135 TAEOTRKLTIDVEAQVLNOTTRLEQLEHSLSTNLKDQNSFLEK 194

Query 162 NLV-----NMNEYDKSVANLTF-----V 183

Query 195 VLAEDKHIIQLOSISIKEKDQLOLVSKQNSITELEKKIVATVRNSVLQKQHDLMET 254

Query 26 MDSIGKKQQVQHGSSYTFLIPEMDNCRSSSPYVNAQDAPLEYDSDYQRLOVLEN 85

Query 85 LKE-----IVNSLKKSCQCCKLQADNGDB3RNLILLPSTGAPGEVGDN -- 128
 Db 86 IMENNTOWLMKLENYIQQNMKKMVEQQNAYQN-----QAVMISIGTLLNC 134

Query 129 -----RVRELESEV-----NKLSSELKNAKEEINVHLGR--JEKL 161
 Db 135 TAEOTRKLTIDVEAQVLNOTTRLEQLEHSLSTNLKDQNSFLEK 194

Query 162 NLV-----NMNEYDKSVANLTF-----V 183

Query 195 VLAEDKHIIQLOSISIKEKDQLOLVSKQNSITELEKKIVATVRNSVLQKQHDLMET 254

Query 184 VNSLDGKCSKCPSEQIORSRPYQHLYKDCDYAAIGKRSSSETYRTDPKNSSFEVYCD 242
 Db 315 MEAGGGGTITQREDGSVDFTWREKVGFGNPSEGYLNEFISOLTNCRYWLKH 374

Query 304 LEDENGVELYDQFYVANEFLKYRLVGVNTAGDALRENKHYNDLKFTTPDKDN 363

Db 375 LKMEWGENAASLYEHPFLSSEEINYLHLKGLTGAKISSISQPGND---FSTRGDN 430

Query 364 DRYFGNGGCGLYSSGWNFDACLSANLNQKYYHQKRYGRVR--NGIFWGWTGPVSEAHPGGYK 422
 Db 433 DKC1C-KCSQMLTGWW#DAGPSNLNGMMYPCRONTNKFN1K1WKG----SGY- 482

Query 422 SSFKEARMIRPKHF 437
 Db 483 -SLKATTMMIRPADF 496

RESULT 13
US-09-561-530-4

Sequence 4, Application US/09561-500

Patent No. 6342119

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

FILE REFERENCE: 4001.002500

CURRENT APPLICATION NUMBER: JS/09/561,500

CURRENT FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR FILING DATE: 1999-04-28

SEQ ID NO 4

LENGTH: 496

TYPE: PRT

ORGANISM: Homo sapiens

US-09-561-500-4

CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432

PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 496

TYPE: PRT

ORGANISM: Homo sapiens

US-09-561-108-4

Query Match 22.0%; Score 522; DB 4; Length 496;
Best Local Similarity 27.9%; Pred. No. 1-2e-39;
Matches 138; Conservative 74; Mismatches 259; Indels 124; Gaps 15;

Qy 43 LERSGKCE---EAGECPYQVSFLPPL----TIQ-LPKQFSRIBEVFKEVQN 84
Db 26 MDS-GKQCYQVQHGSCTYFLPEMNCSSSSSPYVSNAVQDAPLEYCDSVQRQLEN 85

Cy 85 LKE-----IVNSLXKSCQDCDKLOADNGDGPGRNGLLUPSTGAPEGVGN---- 128
Db 26 IMENNTQWMLKLENYIQDNMKKEMVEIQNAVN-----QTAWMBIGTNLNQ 134

Cy 129 -----RVRELESEV-----NKLSSELKNAKEE-NVLHGR--LEKL 161
Db 135 TAEOTRKLTIDVEAQVLNQTTRLEQLEHSLSTNKLEKQILDQTEINLKQQRNSFLEK 194

Cy 162 NLV-----NMNNTENYDVKVANLTF-----V 183
Db 195 VLADEDKHIIQLOSS-KEKEQLOVLVSQNSLIELEKKIVATVNNSVLQKQHDLMET 254

Cy 184 VNLDGKCSKCPSEQIOQRSPVQHLTYKDCSDYYAIGKRSEETYRVPDPKNSSFEVYCD 243
Db 255 VNNLLTMNSTSBAKDPVAKBQISFDCAEVPSHTTNTLYLTFPNSTEI1KAYCD 314

Cy 244 METMGGMWTVQARLGDGSTNFTRTQDYKAGFGNLREFWLGNDKHILJTSKEMILRID 323
Db 315 YEASGGWTITQREDGSVDFTORTWKEYKVGFNPSEYWNLGNEFVSQTLTQCQRYVLIKH 374

Cy 344 LEDPGVLEYALYDQFYVANEFLKYLHVGNVNTAGDALRNQHYNHDLKFTTPDKDN 363
Db 375 LKQEGNRPVLYSSHEFHYSLEHFLSYLQFDTAGKISSISOPGND---ESTXGDN 430

Cy 364 DRYPSGNCGLYSSGKWFDACLSANLNGKYHOKYGRV-NGIFWGT-WPGVSEAHPGCGYK 422
Db 431 DKC1C-KSQMLTGGWWIDACFSNLNGXYYFORQNTNKENGIKWYMWKG----SGY- 482

Cy 423 SSPEAKNMIRPHGF 437
Db 483 -SLKATNMIR2ADP 496

RESULT 15
US-09-351-543-4

Sequence 4, Application US/09351543
Patient No. 6466623

GENERAL INSCRIPTION:

APPLICANT: THORPE, PHILIP E.

APPLICANT: RAN, SOPHIA

TITLE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TO

TITLE OF INVENTION: AMINOPHOSPHOLIPIDS

FILE REFERENCE: 4001.302200

CURRENT APPLICATION NUMBER: JS/09/351-543

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 4

LENGTH: 496

TYPE: PRT

ORGANISM: Homo sapiens

US-09-351-543-4

Query Match: 22.0%; Score 522; DB 4; Length 496;

Best Local Similarity 27.9%; Pred. No. 22e-39; Mismatches 159; Indels 124; Gaps 15;

Matches 138; Conservative 74; N mismatches 159; Indels 124; Gaps 15;	
43 LESRGKCE--EAGECPYQYSPPPL-----TIQ--LPKOFSRIZEEFKEYON 84	
26 MDSIGRKQYQVORGSCSYTFLPENMDNCRSSSPVVSNAVRDAPLEYDOSVSGRJQVDEN 85	
65 LKE-----IVNSLKKSCDCCKLQADDNGCPRGRNGLLPSTGARGEYGN-----128	
86 IMENNTQWLMKGLENYIQDNRMKEMVEICQNANQ-----QTAYMIECTNLNO 214	
129 -----RVERESEV-----NKLSSELXAKAKEEINVHLGR---LEKL 161	
135 TAECTRKLTDVEAQVLNOTTRLEQLHELSUSTNLEKQCLDQ-SEINNLQDKNSPLEKK 194	
162 NLV-----RNQNNIENYVQSKVANLT-----V 183	
195 VLADEDKHTIQLQSIKEEKDOLQVLYSKQNSIIELEKK-VTATVANSVYLQKQGDLYET 254	
184 VNSLUDGKCSKCSCPSCOEIQCSRVPVHLLJKYKDCSDYYIGKRSSETYRVTPDKNSSFENVYCD 243	
255 VNLLTMMSTSNSAKDPTVAKEEQISFRDAEVFKSHTGNGITLTFENSTEIKAYED 31.4	
244 METMGGWTWLQARLDSLNFTRTHODYKAGFGNLRRENLGNDKIHJTKSKEMIJRD 303	
315 XEAGGGWTIQLRREGSVDFRTKEYKVGFGNPSEGZLGNFEPVSQ-TNOORYVLUKH 374	
304 LDFFNSVELAUYDQPYVANEFLKPLJHVNNGTAGDALRFRKHYNMELKFPTDREN 563	
375 LKCWEENEASVYHPLSSEZLNRIELKGLTGAGKISSISQFGND----FS, KODEN 410	
364 DRYPSGNCLGYYSSGMFDAC-SANLNGKYHQKVRGVR-NG1FNGTWPGVSEAHPGSYK 422	
431 DCDC-KCSQMLTGGWFADCGPSNLNGYYPQRCTYNKFNGIKYWWKG----SGY- 482	
423 SSEKEAKMMIRPKHF 437	
Db 483 -SLKATTMMIRPADF 496	

Search completed: November 5, 2003, 16:48:59
 Job time : 32.9427 secs

protein - protein search, using sw model						
on:	November 5, 2003, 16:39:17 ; Search Time 0.92511 Seconds (without alignments; 1559.306 Million cell updates/sec)					
title:	US-09-902-563-18	Score	88	Length	9616862	Database:
Sequence:	.DRYPSGNCGLYSSG 15	Alignments:	1	Start:	1	End:
Scoring table:	BLOSUM62	Gapopen:	10.0	Gapext:	0.5	
Searched:	283308 seqs.	Number of hits satisfying chosen parameters:	283306			
Maximum DB seq length:	0	Maximum Match %:	100%	Number of summaries:	45	
Statistical processing:	Minimum Match %:	Maximum Match %:	100%	Listing first:	45	
Database:	pir1,*	pir2,*	pir3,*	pir4,*		
PiR 76:						
1:	pir1,*					
2:		pir2,*				
3:			pir3,*			
4:				pir4,*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	
1	88	100.0	432	2	I56934	cytobiotin-like protein
2	88	100.0	432	2	A27447	cytotoxic T-lymphocyte protein
3	88	100.0	439	2	I37391	fibrinogen-like protein
4	46	52.3	2403	2	A59386	sanko - human
5	46	52.3	3461	2	S58870	reelin precursor -
6	43	48.9	225	2	C82893	hypothetical protein
7	43	48.9	284	2	I49707	germ cell specific protein
8	43	48.9	339	2	T24007	hypothetical protein
9	43	48.9	456	2	C86624	hypothetical protein
10	43	48.9	456	2	H72000	hypothetical protein
11	42.5	48.3	696	2	G718209	probable outer membrane protein
12	41	46.6	273	2	T-6246	hypothetical protein
13	41	46.6	368	2	A81289	hypothetical protein
14	41	46.6	385	2	T26404	hypothetical protein
15	41	46.6	437	2	A122513	hypothetical protein
16	41	46.6	517	1	ERADA7	early E2A DNA-binding gene P2 protein -
17	41	46.6	591	1	WMBPQ2	outer membrane protein
18	41	46.6	680	2	H70347	xytan 1,4-beta-xylanase
19	41	46.6	798	2	T00131	ferredoxin - Therm
20	40	45.5	92	2	A72242	hypothetical protein
21	40	45.5	106	2	JN0134	hypothetical protein
22	40	45.5	165	2	D86694	early E2A DNA-binding protein
23	40	45.5	245	2	G64210	uracil DNA glycosylase
24	40	45.5	286	2	A33546	actin-capping protein
25	40	45.5	294	2	F03043	calcium-binding protein
26	40	45.5	305	2	F98442	calcineurin (ABC319)
27	40	45.5	455	2	E64154	proline-tRNA ligase
28	40	45.5	474	1	ERAD12	early E2A DNA-binding protein
29	40	45.5	484	1	ERAD11	early E2A DNA-binding protein

3.2	4.0	45.5	490	2	T44576
3.1	4.0	45.5	521	2	D87413
3.2	4.0	45.5	776	2	S28258
3.3	4.0	45.5	1151	2	T19297
3.4	4.0	45.5	1211	2	S54550
3.5	3.9	44.3	117	2	128135
3.6	3.9	44.3	118	2	S25051
3.7	3.9	44.3	155	2	JH0226
3.8	3.9	44.3	155	2	JH0227
3.9	3.9	44.3	155	2	JS0657
4.0	3.9	44.3	156	1	UQ70A
4.1	3.9	44.3	156	2	S25305
4.2	3.9	44.3	156	2	T52314
4.3	3.9	44.3	156	2	T52315
4.4	3.9	44.3	157	2	D36571
4.5	3.9	44.3	157	2	C36571

ALIGNMENTS

卷之三

length: 0

```

    - 156934
      fibrinogen-like protein - mouse
      CSpecies: Mus sp. (mouse)
      CDate: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
      CAccesion: I56934
      RParr, R.L.; Fung, L.; Reneker, J.; Myers-Masch, N.; Leibowitz, J.Z.; Levy, G.
      J.Viro. 69, 5033-5036, 1995
      ATitle: Association of mouse fibrinogen-like protein with murine hepatitis virus
      AReference number: 256934; MJD:9533285; PMID:7609073
      AAccesion: I56934
      AStatus: preliminary; translated from GB/EMBL/DDJB
      AMolecule type: mRNA
      AResidues: 432 <RES>
      ACrossReferences: GB:S78773; NCBI:AC42169; PID:NAA334823; 1; PDB:9421770
      Pred. No. is the number of results predicted by chance to have a

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IMMUNITIES

SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	Best Local Similarity	Score	DB 2; Length	Details
1	88	100.0	432	2 156934	fibrinogen-like protein precursor (clone pT49); - mouse	100.0%	Score 88;	DB 2; Length 432;	
1	88	100.0	432	2 A27447	cytotoxic T-lymphocyte-specific protein precursor (clone pT49); - mouse	100.0%	Pred. No. 2.1e-06;		
2	98	100.0	439	2 137391	fibrinogen-like protein precursor - human	100.0%	Mismatches 0;		
3	98	100.0	439	2 A59386	sarko - human	100.0%	C; Indels 0;		
4	46	52.3	24C3	2 52.3	hypothetical protein precursor -	100.0%	Gaps 0;		
5	46	52.3	3461	2 C82893	hypothetical protein precursor -	100.0%			
6	43	48.9	225	2 C82893	hypothetical protein precursor -	100.0%			
7	43	48.9	284	2 I49707	hypothetical protein precursor -	100.0%			
8	43	48.9	339	2 T24007	hypothetical protein precursor -	100.0%			
9	43	48.9	456	2 C86624	hypothetical protein precursor -	100.0%			
10	43	48.9	456	2 H72000	hypothetical protein precursor -	100.0%			
11	42.5	49.3	696	2 G71829	probable outer membrane protein	100.0%			
12	41	46.6	273	2 T-6246	hypothetical protein precursor -	100.0%			
13	41	46.6	368	2 A81289	hypothetical protein precursor -	100.0%			
14	41	46.6	285	2 T26404	hypothetical protein precursor -	100.0%			
15	41	46.6	437	2 A12513	hypothetical protein precursor -	100.0%			
16	41	46.6	517	1 ERADA7	early E2A DNA-bind gene P2 protein -	100.0%			
17	41	46.6	591	1 WNPQ02	outer membrane protein	100.0%			
18	41	46.6	680	2 H70347	xyan 1,4-beta-D-xylose reductase - Therm	100.0%			
19	41	46.6	798	2 T00131	hypothetical protein precursor -	100.0%			
20	40	45.5	92	2 A72242	hypothetical protein precursor -	100.0%			
21	40	45.5	100	2 JR0734	hypothetical protein precursor -	100.0%			
22	40	45.5	165	2 D66894	uracil DNA glycosylase -	100.0%			
23	40	45.5	245	2 G54210	actin-capping protein	100.0%			
24	40	45.5	286	2 A35546	calcium-binding protein	100.0%			
25	40	45.5	294	2 AF1043	regecacin (AB0379)	100.0%			
26	40	45.5	305	2 F08242	proline-tRNA ligase	100.0%			
27	40	45.5	455	2 B64454	early E2A DNA-bind	100.0%			
28	40	45.5	474	1 ERAD12	early E2A DNA-bind	100.0%			
29	40	45.5	484	1		100.0%			

DD 357 DRYPSGNCGLYSSG 374

RESULT 3
 A: Molecule type: mRNA
 A: Residues: T-215; 'T', 217-1905; 'S', 1907-3355; 'V', 3357-3391; 'N', 3393-3461 <DA2>
 C: Cross-references: EMBL:U24703; NID:902486; PID:gi02487
 C: Superfamily: unassigned EGF-related proteins: EGF homology
 F: 1-27/Domain: signal sequence #status predicted <SIG>
 F: 28-346/Product: reelin #status Predicted <MAT>
 F: 1169-1795/Domain: EGF homology <EGF>

Query Match Score 46; DB 2; Length 3461;
 Best Local Similarity 71.4%; Pred. No. 76;
 Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 3 YPSGNCGLY--YSS 14
 Db 1974 YPGK-GLYCPYSS 1987

RESULT 4
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Residues: 1-439 <RES>
 A: Note: submitted to the EMBL Data Library; August 1994
 C: Superfamily: fibrinogen gamma chain: fibrinogen beta/gamma homology <FBG>
 F: 216-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match Score 88; DB 2; Length 439;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPSGNCGLYSSG 15
 Db 364 DRYPSGNCGLYSSG 378

RESULT 5
 A59386 - human
 C: Species: Homo sapiens (man)
 C: Date: 31-Dec-2001 #sequence_revision: 31-Dec-2001 #text_change 31-Dec-2001:
 C: Accession: A59386
 C: Reference number: A59386
 A: Status: preliminary
 A: Molecule type: protein
 A: Residues: 1-2403 <SAN>

Query Match Score 46; DB 2; Length 2403;
 Best Local Similarity 64.3%; Pred. No. 54; Mismatches 1; Indels 2; Gaps 1;

Qy 4 PSGNC3-LYYSSG 15
 Db 1752 PSSNGGFLFYSSG 1765

RESULT 6
 A59386 - human
 C: Species: Ureaplasma urealyticum
 C: Date: 18-Aug-2000 #sequence_revision: 20-Aug-2000 #text_change 20-Aug-2000
 C: Accession: C82893
 R: Glass, J.J.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, S.Y.; Casselli, G.H.
 Submitted to GenBank, February 2000
 A: Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a t
 A: Reference number: A92870
 A: Accession: C82893
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-225 <GLA>
 A: Cross-references: GB:AE002139; GB:AF222894; NID:96899405; PID:AAF30837.1; GSPDB:GN0
 A: Experimental source: serovar 3; biovar 1
 C: Genetics:
 A: Gene: U425
 A: Genetic code: SG3

Query Match Score 48.9%; DB 2; Length 225;
 Best Local Similarity 70.0%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YPSGNCGLY 12
 Db 87 YPENGNAELY 96

RESULT 7
 A59386 - mouse
 C: Species: Mus musculus (house mouse)
 C: Date: 23-May-1998 #sequence_revision: 29-May-1998 #text_change 19-May-2003
 C: Accession: 149707
 R: Tanaka, H.; Yoshimura, Y.; Nishina, Y.; Nczaki, M.; Nishimura, Y.
 FEBS Lett. 355, 4-10, 1994
 A: Title: Isolation and characterization of cDNA clones specifically expressed in testi
 A: Reference number: 149707; PMID:95046372;
 A: Accession: 149707
 A: Status: preliminary; translated from GB/EML/DBJ
 A: Molecule type: mRNA
 A: Residues: 1-284 <RES>
 A: Accession: GB:D38545; NID:9603492; PID:gi603493
 A: Cross-references: GB:D38545; NID:9603492; PID:gi603493
 C: Superfamily: actin-capping protein alpha chain

Query Match Score 48.9%; DB 2; Length 284;
 Best Local Similarity 60.0%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DRYPSGNCG 10
 Db 132 DHYPNGNCIV 140

RESULT 8
 A59386 - mouse
 C: Species: Mus musculus (house mouse)
 C: Date: 06-Dec-1996 #sequence_revision: 06-Dec-1996 #text_change 11-Jan-2000
 C: Accession: S58870; S71844; I42297
 R: D'Arcangelo, G.; Miao, G.G.; Chen, S.C.; Soares, H.D.; Curran, T.
 Nature 374, 719-723, 1995
 A: Title: A protein related to extracellular matrix proteins deleted in the mouse mutant
 A: Reference number: 149297; NID:95211649; PMID:775726
 A: Status: nucleic acid sequence not shown
 A: Molecule type: mRNA
 A: Residues: 1-3461 <DAR>
 A: Cross-references: EMBL:U24703; NID:9902486; PID:gi9902487
 R: D'Arcangelo, G.
 Submitted to the EMBL Data Library, April 1995
 A: Reference number: S71844
 A: Accession: S71844

C.1. Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolcay, J.; McClarty, G.; Saizter, Nucleic Acids Res. 28, 1397-1406, 2000
 A.Species: *Caenorhabditis elegans*
 A.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 A;Accession: T24007
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-456 <REAA>
 A;Cross-references: GB:AE002238; PID:AE002161; MID:97189633; PIDN:AF38579.1; PMID:1064935
 A;Experimental source: strain AR39, HL cells
 C;Genetics:
 A;Gene: CPn1070; CP0780

Query Match 48.9% Score 43; DB 2; Length 456;
 Best Local Similarity 60.0%; Pred. No. 34; Mismatches 3; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YPGNCGLYXX 12
 Db 3 FPGKNCXY 12

RESULT 1:
 G11829
 probable outer membrane protein - *Helicobacter pylori* (strain 299)
 C;Species: *Helicobacter pylori*
 A;Variety: strain J99
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
 C;Accession: G71829; G71960
 C;Alt. Accession: R.A.; Liss, L.S.L.; Mcir, D.T.; King, S.D.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Neberg, B.; Willis, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.
 Nature 397, 776-80, 1999
 A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen
 A;Reference number: A11800; MUID:99120557; PMID:9923682
 A;Accession: G71829
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-696 <ARN>
 A;Cross-references: GB:AE001549; PIDN:ADD6834.1; PID:94155888; MID:94155889; PID:94155890
 A;Experimental source: strain J99
 A;Accession: G71829
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-696 <ARN>
 A;Cross-references: GB:AE001459; PIDN:ADD5786.1; PID:94154
 A;Experimental source: strain J99
 C;Genetics:
 A;Gene: Jhp0212

Query Match 48.3% Score 43; DB 2; Length 696;
 Best Local Similarity 69.2%; Pred. No. 61; Mismatches 3; Indels 1; Gaps 1;
 Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 3 YPGNCGLYXX 15
 Db 3 YPGCN-GNYSSG 242

RESULT 12:
 T16246
 hypothetical protein F35A5.4 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
 C;Accession: T16246
 R;Leimbach, D.
 submitted to the EMBL Data Library, January 1996
 A;Description: The sequence of *C. elegans* cosmid F35A5.
 A;Accession: T16246
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-273 <DNA>
 A;Cross-references: EMBL:U46675; PID:9116614; PIDN:AB52645.1; GSPDB:GN
 A;Experimental source: strain Bristol N2; clone F35A5.
 C;Genetics:

RESULT 10:
 T172000
 hypothetical protein CP0780 [imported] - *Chlamydophila pneumoniae* (strains CWL529 and AR39)
 C;Species: *Chlamydophila pneumoniae*, *Chlamydia pneumoniae*
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C;Accession: H72000; A81538
 R;Kalmus, S.; Mitchell, W.; Marathe, R.; Zammel, C.; Fan, C.; Clinger, L.; Grimwood, C.; Nature Genet. 21, 385-389, 1999
 A;Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.
 A;Reference number: A72000; MUID:99206666; PMID:10192388
 A;Accession: H72000
 A;Molecule type: DNA
 A;Residues: 1-456 <ARN>
 A;Cross-references: GB:AE001687; GB:AE001363; NID:94377395; FIDN:ADD19207.1; PID:9437740
 A;Experimental source: strain CWL029
 R;Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.E.; White, O.; Hickey, C;Genetics:

A;Gene: CESP:F35A5.4
 A;Map position: X
 A;Introns: 18/3; 62/3; 81/3; 100/3; 140/3; 226/2
 Query Match 46.6%; Score 41; DB 2; Length 273;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 PSENCGLYSSG 15
 Db 50 PSENCGGSGSG 61

RESULT 13

A81289 hypothetical protein Cj143c [imported] - Campylobacter jejuni [strain: KCTC 1168]
 C;Species: Campylobacter jejuni
 C;Cross-references: DDBJ/APCC0063; PIDN:BA81C89.1; P2D:95105777
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C;Accession: A7513
 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-nc, K.; Takeuchi, H.; Takamatsu, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyperthermophilic Crenarchaeon, Aeroflynnia sp. strain K1
 A;Reference number: A72450; MUID:39310339; SMID:10382566
 A;Accession: A7513
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-437 <RAW>
 A;Cross-references: DDBJ/APCC0063; PIDN:BA81C89.1; P2D:95105654
 A;Experimental source: strain: K1
 C;Genetics:

A;Gene: APE2078
 C;Superfamily: conserved hypothetical protein YTH1394
 C;Query Match: 46.6%; Score 41; DB 2; Length 437;
 Best Local Similarity 57.1%; Pred. No. 69;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 RYPSGNGLYSSG 15
 Db 112 RYFEGEAGLTLSSG 125

Search completed: November 5, 2003, 16:48:15
 Job time : 2.92511 secs

A;Gene: Cj143c
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-368 <PAR>
 A;Cross references: GB:ALL139078; GB:ALL11168; NID:96968723; PIDN:CAB73857.1; PID:3696886
 A;Experimental source: serotype C2, strain NCIC 1168
 C;Generics:
 A;Gene: Cj143c
 C;Superfamily: Campylobacter jejuni hypothetical protein Cj1433c
 C;Query Match 46.6%; Score 41; DB 2; Length 368;
 Best Local Similarity 70.0%; Pred. No. 59;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 PSENCGLYS 13
 Db 265 PSENCDVHS 274

RESULT 14

T26404 hypothetical protein Y105CSB.bb - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Cross-references: T26404
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C;Accession: T26404
 R;McMurray, A.
 submitted to the EXBL Data Library, September 1999
 A;Reference number: Z202C8
 A;Accession: T26404
 A;Title: preliminary: translated from GS/EYBL/DCBC
 A;Molecule type: DNA
 A;Residues: 1-105 <WIL>
 A;Cross-references: EML:ALL10479; PIDN:CA:BS4376.1; CESPD:Y105CSB.bb
 C;Generics:
 A;Gene: CESPY:Y105CSB.bb
 A;Introns: 58/1; 112/1; 270/2
 C;Superfamily: glutamate-ammonia ligase

Qy 1 DRYPSGNCGIYSSG 15
 Best Local Similarity 53.3%; Pred. No. 61;
 Matches 8; Conservative 1; Mismatches 6; Indels 2; Gaps 0;

Db 341 DRRPSSNCDFYTVTG 255

RESULT 15

protein - protein search, using sw model						
on: November 5, 2003, 15:59:02 ; search time 0.560793 Seconds (without alignments) 1067.506 Million cell updates/sec						
Title: US-09-902-563-18						
Refact score: 8.8						
Sequence: 1 DRVFSGNCCJYVYSSG 15						
Scoring table: BLOSUM62						
Gapext: 0.5						
Searched: 127863 seqs, 47626705 residues						
Total number of hits satisfying chosen parameters:						127863
Minimum DB seq length: 6						
Maximum DB seq length: 2000000000						
Post-processing: Minimum Match 9%						
Post-processing: Maximum Match 100%						
Listing first 45 summaries						
Database: Swissprot_41::						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query	Match	Length	DB ID	Description
1	88	100.0	432	1	FGL2_MOUSE	PI2684 mus musculus
2	88	20.0	439	1	FGL2_HUMAN	Q14314 homo sapiens
3	46	52.3	3209	1	RELN_CHICK	Q93574 gallus gallus
4	46	52.3	3460	1	RELN_HUMAN	P778539 homo sapiens
5	46	52.3	3461	1	RELN_BOVINE	Q60841 mus musculus
6	46	52.3	3462	1	RELN_RAT	P58751 rattus norvegicus
7	45	51.1	210	1	BCA3_HUMAN	Q9ndq1 homo sapiens
8	45	48.9	299	1	BCA3_HUMAN	Q96x22 homo sapiens
9	43	48.9	299	1	CAZ3_MOUSE	P70183 mus musculus
10	43	48.9	299	1	CAZ3_RAT	Q9wv4y rattus norvegicus
11	42	46.6	121	1	CHA1_LYMPDI	P506C3 lymphocyte
12	42	46.6	437	1	YK78_AERPE	Q9ya6G aeropyrum
13	42	46.6	498	1	CTAC_HUMAN	Q96m04 homo sapiens
14	42	46.6	517	1	DNB2_ADE07	P04497 human adenocarcinoma
15	41	46.6	590	1	VPC2_BPPRD	P227372 bacteriophage
16	40	45.5	245	1	UNG_XYCGE	P47343 mycoplasma
17	40	45.5	286	1	CAZ1_CHICK	P13127 gallus gallus
18	40	45.5	435	1	SYP2_METJA	Q56635 methanococcus
19	40	45.5	474	1	DNB2_ADE41	P11807 human adenocarcinoma
20	40	45.5	484	1	DNB2_ADE12	P04498 human adenocarcinoma
21	40	45.5	776	2	ADC7_MACPA	Q28475 macaca fasciata
22	40	45.5	121	1	ATH1_YEAST	P48016 saccharomyces
23	39.5	44.3	1391	1	LYS2_CENAL	Q12572 candida albicans
24	39	44.3	78	1	R27A_ASPOF	P31753 aspergillus
25	39	44.3	79	1	R27A_HORVU	P22277 hordeum vulgare
26	39	44.3	79	1	R27A_MAIZE	P27992 zea mays
27	39	44.3	80	1	R27A_LYCES	P27083 lycopersicon esculentum
28	39	44.3	81	1	27AB_ARATH	P59232 arabidopsis thaliana
29	39	44.3	81	1	27AC_ARATH	P59233 arabidopsis thaliana
30	39	44.3	212	1	BCA3_MOUSE	Q9jjs1 mus musculus
31	39	44.3	420	1	Y461_SYNY3	Q55167 synechocystis sp
32	39	44.3	754	1	AD07_HUMAN	Q9h2u9 homo sapiens
33	39	44.3	832	1	SM48_HUMAN	Q9npr2 homo sapiens

DR	SMART:SM00186; FBG1; PROSINE; PS00514; FIBRIN AG_C DOMAIN; 1.	RA	Whiting N., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scnemer A., Schein J.B., Jones S.J.M., Marrs M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16809-16903 (2002).
RN	T-cell; Cytolysis; Signal.	FT	POTENTIAL.
FT	SIGNAL 1 19	FT	FIBROLEUKIN
FT	CHAIN 2C 432	FT	FIBRINOGEN C-TERMINAL.
FT	DOMAIN 203 428	FT	BY SIMILARITY.
FT	DISULFID 206 235	FT	BY SIMILARITY.
FT	DISULFID 364 377	FT	BY SIMILARITY.
FT	CARBONYD 24 24	FT	(POTENTIAL).
FT	CARBONYD 172 172	FT	N-LINKED (GLCNAC).
FT	CARBONYD 228 228	FT	(POTENTIAL).
FT	CARBONYD 256 256	FT	N-LINKED (GLCNAC).
FT	CARBONYD 329 329	FT	(POTENTIAL).
FT	CONFLICT 332 332	FT	N-LINKED (GLCNAC).
FT	SEQUENCE 432 AA; 48951 MW;	FT	A > G (IN REF 2).
FT	2B29/PF69CCB4A782 CRC64;	FT	(POTENTIAL).
Query Match	Best Loca: Similarity 100.0%; Fred. No: 8.2e-07; Length 432;	CC	
Matches 15;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	
Qy	1 DPVPSGNCGYSSG 15	CC	
Db	357 DPVPSGNCGLYSSG 371	CC	
RESULT 2		CC	
ID	FGL2_HUMAN STANDARD;	FT	439 AA.
AC	Q14314;	FT	Created:
DT	16-OCT-2001 (Rel. 40)	FT	Last sequence update:
DT	16-OCT-2001 (Rel. 40)	FT	Last annotation update:
DT	15-SEP-2003 (Rel. 42)	FT	Last annotation update:
DE	Fibroleukin precursor (Fibrinogen-like protein; 2) (pt19).	FT	
GN	EG2.	FT	
CS	Homo sapiens (Human); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT	
CC	CC	FT	
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homidae.	FT	
CX	NCB:TaxID:9606;	FT	
RN	11]	FT	
RP	SEQUENCE FROM N.A.	FT	
RC	TISSUE:Small intestine;	FT	
RC	MEDLINE=95569700; PubMed=7642-06;	FT	
RA	Fueegg C., Pytel A.R.;	FT	
RT	"Sequence of a human transcript expressed in T-lymphocytes and encoding a fibronogen-like protein";	FT	
RT	Gene 16G:257-262(1995).	FT	
RJ	12]	FT	
RP	SEQUENCE FROM N.A.	FT	
RA	Yuvaraj S., Liu M., Yarsden P., Levy G.;	FT	
RA	"Cloning and characterization of Hg912: the human counterpart to the mouse gene EG12";	FT	
RT	Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.	FT	
RN	13]	FT	
RP	SEQUENCE FROM N.A.; AND VARIANT GLU-53.	FT	
RA	Rieder M.C., Arce T.Z., Carrington D.P., Chung M.-W., Lee K.-J., Poel C.L., Ozuna M., Y. Q., Kickerton D.A., Submitted (JAN-02) to the EMBL/GenBank/DDBJ databases.	FT	
RN	14]	FT	
RP	SEQUENCE FROM N.A.	FT	
RC	TISSUE:Blood;	FT	
RX	STRausberg R.J., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Cojins F.S., Wagner L., Stenner C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat K.K., Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., McDonald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carnicelli P., Prange C., Pahna S.S., Loquaiano N.A., Peeters G.J., Abramson R.D., Gunarane P.H., Bosak S.A., McEvian P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Say I.J., Fully S.W., Villaion D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	RA	Query Match: 100.0%; Score 88; DB: 1; Length 439; Best Local Similarity 100.0%; Pred. No: 8.3e-07; Matches 15; Conservative 0; Mismatches 0; indels 0; Caps 0;
Qy	: DRYPSGNCGLYSSG 376	CC	
Db	: DRYPSGNCGLYSSG 376	CC	
RESULT 3		CC	

REELIN-CHICK	STANDARD;	PRT;	3209 AA.	
NCBI_TaxID:903574;				
DOC	28-FEB-2003 (Ref.: 41, Created)	FT;	41	
DOC	28-FEB-2003 (Ref.: 41, Last sequence update)	FT;	41	
DOC	28-FEB-2003 (Ref.: 41, Last annotation update)	FT;	41	
REELIN	Reelin (EC 3.4.21.-) (Fragment).			
NCBI_TaxID:9031;				
SEQUENCE FRCM N A				
Bernier B., Goffinet A.M.;	Comparative study of reelin in vertebrates.;			
Submited (SREP-998) to the EMBL/Genbank/DBU databases				
-: FUNCTION: Extracellular matrix serine protease that plays a role				
in layering of neurons in the cerebral cortex and cerebellum.				
Regulates microtubule function in neurons and neuronal migration.				
Affects migration of sympathetic preganglionic neurons in the				
spinal cord, where it seems to act as a barrier to neuronal				
migration. Enzymatic activity is important for the modulation of				
cell adhesion. Binding to the extracellular domains of lipoprotein				
receptors VLDLR and APOE2 induces tyrosine phosphorylation of				
Dab1 and modulation of Tau phosphorylation (By similarity).;				
-!- SUBUNIT: Binds to the ectodomains of VLDLR and APOE2 (By				
similarity).				
-!- SUBCELLULAR LOCATION: Secreted (By similarity).				
-!- DOMAIN: The basic C-terminal region is essential for secretion (By				
SIMILARITY):				
-!- SIMILARITY: BELONGS TO THE REELIN FAMILY.				
-!- SIMILARITY: Contains 8 EGF-like domains.				
-!- SIMILARITY: Contains 15 BNR repeats.				

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modified and this statement is not removed. Usage by and for commercial				
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or send an email to license@ebi.ac.uk).				

EMBL: AF090441; AAC35559; 1. -				
HSSP: P05106; JYV2.				
InterPro; IPR006229; EGF like.				
InterPro; IPR00240G; GH_BNR.				
InterPro; IPR00621C; -EGF.				
PFAM; PF02012; BNF_15.				
PFAM; PF00240G; EGF_I_4.				
SMART; SMC0181; EGF_I_5.				
PROSITE; PS00022; EGF_I_7.				
PROSITE; PS01186; EGF_I_7.				
Hydrolase; Serine protease; Developmental protein; Matrix protein;				
Cell adhesion; EGF-like domain; Glycoprotein; Repeat.				
NON_TER	1			
DOMAIN	418	EGF LIKE 1.		
DOMAIN	777	EGF-LIKE 2.		
DOMAIN	1157	EGF-LIKE 3.		
DOMAIN	1513	EGF-LIKE 4.		
DOMAIN	1877	EGF-LIKE 5.		
DOMAIN	2226	EGF-LIKE 6.		
DOMAIN	2601	EGF-LIKE 7.		
DOMAIN	2776	EGF-LIKE 8.		
REPEAT	340	BNR 1.		
REPEAT	546	BNR 2.		
REPEAT	699	BNR 3.		
REPEAT	904	BNR 4.		
REPEAT	1070	BNR 5.		
REPEAT	1283	BNR 6.		
REPEAT	1434	BNR 7.		
REPEAT	1632	BNR 8.		

SEQUENCE OF 194-2556 FROM N A				
RX	Lamar B., Wamsley P., Gibson A., Maas J., Bauer C., Sapptti L.;			
RA	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.			
RN [3]				
RP	ALTERNATIVE SPLICING.			
RX	Medline:99233436; PubMed:10328932;			
RA	Lambert de Rouvroit C., Bernier B., Royaux I., de Bergereck V.,			
RA	Goffinet A.M.;			
RA	"Evolutionarily conserved, alternative splicing of reelin during			
RT	development".			
RT	Exp. Neurol. 156:229-238 (1999).			
RN [4]				
RP	DISEASE, AND TISSUE SPECIFICITY			
RX	Medline:59080080; PubMed:9461036.			

RA Impagnatiello F., Guidotti A.R., Pesold C., Dwivedi Y., Caruncho H., Pisu M.G., Uzurov D.P., Smalheiser N.R., Davis J.M., Pandey G.N., Pappas G.D., Tuering P., Sharma R.P., Cottet E.; RT A decrease of reelin expression as a putative vulnerability factor in schizophrenia."; RT *Proc. Natl. Acad. Sci. U.S.A.* 95:15718-15723 (1998). [5] RN [6].

RF DISEASE; RX MEDLINE=202890; PubMed=10973357;

RA Hong S.E., Shugart Y.Y., Huang D.T., Shahwan S.A., Grant P.E., Hourihan J.O.B., Martin N.C.F., Kash C.A.; RT associated with human REELN mutations."; RT Nat. Genet. 26:93-96 (2000).

RN [7].

RF DISEASE; RX MEDLINE=2127116; PubMed=11317216;

RA Persico A.M., D'Agruma L., Maiorano N., Totaro A., Mittereri R., Savarino C., Wessink T.H., Schneider C., Weilmeier R., Trifilio S., Montecchio F., Palermo M., Pascucci T., Pascucci-Allegra S., Reicheit K.-L., Conciatori M., Yarirc R., Quattrocchi C.C., Baldi A., Belante Z., Gasparini P., Kettler F.; RT Reelin gene alleles and haplotypes as a factor predisposing to autistic disorder"; RT *J. Psych.* 6:150-159 (2003).

CC FUNCTION: Extracellular matrix serine protease that plays a role in layering of neurons in the cerebral cortex and cerebellum. Regulates microtubule function in neurons and neuronal migration. Affects migration of sympathetic preganglionic neurons in the spina cord, where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors VLDLR and ApoER2 induces tyrosine phosphorylation of Dab1 and modulation of Tau phosphorylation (By similarity). CC SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2 (By similarity).

CC SUBCELLULAR LOCATION: Secreted (By similarity).

CC ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=3; Name=1; IsoId=p78509-1; Sequence=Displayed.

CC Name=2; IsoId=p78509-2; Sequence=VSP_005575;

CC IsoId=p78509-3; Sequence=VSP_005576;

CC TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis by the Cajal-Retzius cells and other pioneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layer of the cerebellum. In adult brain, preferentially expressed in GABAergic interneurons of prefrontal cortex, temporal cortex, hippocampus and glutamatergic granule cells of cerebellum. Also expressed in fetal and adult liver.

CC DEVELOPMENTAL STAGE: Expressed in fetal and postnatal brain and liver. Expression in postnatal human brain is high in the cerebellum.

CC DOMAIN: The basic C-terminal region is essential for secretion. By similarity.

CC DISEASE: Defects in REIN are the cause of autosomal recessive lisencephaly with cerebellar hypoplasia (Also known as Norrbottero's syndrome). Some patients also displayed persistent lymphedema neonatalis, and one showed accumulation of chylomicrons (fatty) vesicles fluid.

CC DISEASE: Defects in REIN may contribute to susceptibility to schizophrenia. Expression of the protein is reduced (about 50%) in patients with schizophrenia.

CC DISEASE: Defects in REIN may predispose to autistic disorder. A polymorphic GGC triplet repeat located in the 5'UTR region of REIN (8 to 10 repeats) in the normal population is significantly

increased in autistic patients (4 to 23 additional repeats).

CC -!- SIMILARITY: BELONGS TO THE REELIN FAMILY.

CC -!- SIMILARITY: Contains 8 EGF-like domains.

CC -!- SIMILARITY: Contains 15 BNR repeats.

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CC EMBL; J79716; AAC51105.1; -.

DR EMBL; AC000121; AAB46357.1; -.

DR HSSP; P05106; JVJ27.1; -.

DR Genew; HGNC:9957; REIN.

DR MIN; 6C0514; -.

DR MIN; 25332C; -.

DR InterPro; IPR036209; EGF like.

DR InterPro; IPR0286C; GH_EGN.

DR InterPro; IPR00621C; EGP.

DR InterPro; IPR030261; Reelin.

DR PTSM; PR032012; BNR; 15.

DR PTAM; PR030093; EGF; 4.

DR PTAN; PFC2014; Reeler; 1.

DR SMART; SM0018; EGF; 5.

DR PROSITE; PS00022; EGF; 1.

DR PROSITE; PS0186; EGF; 6.

KW Hydrolase; Serine Protease; Developmental Protein; Matrix protein; Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal; Alternative splicing; Lissencephaly.

FT SIGNAL; 1 25 POTENTIAL.

FT CHAIN; 26 3460 REELIN.

FT DOMAIN; 39 17 EGF-LIKE 1.

FT DOMAIN; 670 701 EGF-LIKE 1.

FT DOMAIN; 1029 1060 EGF-LIKE 2.

FT DOMAIN; 1408 1441 EGF-LIKE 3.

FT DOMAIN; 1764 1795 EGF-LIKE 4.

FT DOMAIN; 2128 2160 EGF-LIKE 5.

FT DOMAIN; 2477 2508 EGF-LIKE 6.

FT DOMAIN; 2852 2883 EGF-LIKE 7.

FT DOMAIN; 3227 3259 EGF-LIKE 8.

FT REPEAT; 592 602 BNR 1.

FT REPEAT; 798 809 BNR 2.

FT REPEAT; 951 962 BNR 3.

FT REPEAT; 1156 1167 BNR 4.

FT REPEAT; 1322 1333 BNR 5.

FT REPEAT; 1534 1545 BNR 6.

FT REPEAT; 1685 1696 BNR 7.

FT REPEAT; 1883 1894 BNR 8.

FT REPEAT; 2042 2053 BNR 9.

FT REPEAT; 2249 2260 BNR 10.

FT REPEAT; 2398 2409 BNR 11.

FT REPEAT; 2597 2608 BNR 12.

FT REPEAT; 2777 2788 BNR 13.

FT REPEAT; 2978 2998 BNR 14.

FT DOMAIN; 3362 3373 N-LINKED (GLCNAC, .) (BASIC).

FT CARBOHYD; 3431 3460 ARG-RICH (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 140 140 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 257 257 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 289 289 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 305 305 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 628 628 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 1266 1266 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 1599 1599 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 1749 1749 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 1920 1920 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 2144 2144 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 2268 2268 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 2316 2316 N-LINKED (GLCNAC, .) (POTENTIAL).

FT CARBOHYD; 2568 2568 N-LINKED (GLCNAC, .) (POTENTIAL).

FT	CARBOHYD	2961	2961	N-LINKED (GLCNAC, ., .)	(POTENTIAL);	Sakai K., Okido T., Furuno K., Aono H., Baldarelli R., Barron G., Blaize C., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita Y., Gariboldi V., Gustincich S., Hill D., Hofmann Y., Hurni D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Massarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shitara K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Synshaw-Boris A., Yoshida K., Hassgawa Y., Kawaji H., Kohotsuki S., Hayashizaki Y., Functional annotation of a full-length mouse cDNA collection.";
FT	CARBOHYD	3015	3015	N-LINKED (GLCNAC, ., .)	(POTENTIAL);	RA
FT	CARBOHYD	3072	3072	N-LINKED (GLCNAC, ., .)	(POTENTIAL);	RA
FT	CARBOHYD	3184	3184	N-LINKED (GLCNAC, ., .)	(POTENTIAL);	RA
FT	CARBOHYD	3411	3411	N-LINKED (GLCNAC, ., .)	(POTENTIAL);	RA
FT	VARSPLIC	3438	3438	N-LINKED (GLCNAC, ., .)	(POTENTIAL);	RA
FT	VARSPLIC	3428	3429	Missing (in isoform 2); /PMID:VSP_005575.	Missing (in isoform 3); / PMID:VSP_005575.	RA
FT	VARSPLIC	3428	3460	Missing (in isoform 3); / PMID:VSP_005575.	Missing (in isoform 3); / PMID:VSP_005575.	RA
FT	CONFLICT	752	752	E -> D (IN REF. 2).	RT	
SEQUENCE	3460 AA;	388199 MW;	BB2C0BA415AB93C; C2C64;	RT		
Cy	3 YPSGNCGLY-YSS 14	52-31%	Score: 46; DB: 1; Length: 3460; Best Local Similarity: 71.4%; Pred. No.: 37%; Mismatches: 0; Indels: 2; Gaps: 1;	RT		
Db	1973 YPGGNGLYCPYSS 1986	52-31%	Score: 46; DB: 1; Length: 3460; Best Local Similarity: 71.4%; Pred. No.: 37%; Mismatches: 0; Indels: 2; Gaps: 1;	RT		
RESULT ⁵	RELN_MOUSE STANDARD; PRT; 3461 AA.	RP				
AC	Q60841; Q9CUA6;	RP				
DT	28-Feb-2003 (Rel. 41; Created)	RP				
DT	28-Feb-2003 (Rel. 41; Last sequence update)	RP				
DT	28-Feb-2003 (Rel. 41; Last annotation update)	RP				
DE	Reelin precursor (EC 3.4.21.-) (Reeler protein).	RP				
GN	RELN CR RL.	RP				
OS	Mus musculus (Mouse); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Xurinae; Yus.	RP				
OC		RP				
CC		RP				
CX		RP				
RN	[1] _taxid=103090;	RP				
RP	SEQUENCE FROM N.A. (ISOFCRM 1).	RP				
RC	TISSUE=Correllum; Miao G.G., Chen S.-C., Soares H.D., Morgan J.T., D'Arcangelo G., Curran T.; "A protein related to extracellular matrix proteins deleted in the mouse mutant reeler."	RP				
RT	"The reeler gene encodes a protein with an EGF-like motif expressed by pioneer neurons."	RP				
RL	Nature 374:719-723(1995). [2]	RP				
RP	SEQUENCE FROM N.A. AND ALTERNATIVE SPlicing.	RP				
RX	XREF="8086481; PubMed=94-7911;	RP				
RA	Royaux I., Lambert de Rouvroit C., D'Arcangelo G., Demirov D., Goffinet A.M., "Genomic organization of the mouse reelin gene.";	RP				
RA	Genomics 46:240-250(1997).	RP				
RN	[3]	RP				
RP	SEQUENCE OF 2152-3461 FROM N.A. (ISOFORM 1).	RP				
RC	STRAIN=BALB/C; TISSUE=Brain;	RC				
RX	MEDLINE=25375189; PubMed=7647795;	RX				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Takahara T., Sasaki N., Hirose K., Yoshiki A., Nakao K., Katsuki M., Murakami Y., Watanabe S., Aizawa T., Okazaki Y., Nishi K., Kyosawa H., Konno S., Yamamoto I., Saito T., Okazaki T., Gotoh T., Bono H., Kasumi S., Saito R., Kadoma K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T., Fleischmann W., Gaasterland T., Grossi C., King B., Kochiwa H., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,	RA				
RX	MEDLINE=21085660; PubMed=11217851;	RA				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa T., Okazaki Y., Nishi K., Kyosawa H., Konno S., Yamamoto I., Saito T., Okazaki T., Gotoh T., Bono H., Kasumi S., Saito R., Kadoma K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T., Fleischmann W., Gaasterland T., Grossi C., King B., Kochiwa H., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,	RA				
RA	Name=1;	RA				
RA	Isoid=Q60841-1; Sequence=Displayed;	RA				
CC	Name=2;	CC				
CC	Isoid=Q60841-2; Sequence=VSP_005577;	CC				

CC Name=j; CC -; TISSUE SPECIFICITY: The major Isoform 1 is neuron-specific. It is abundantly produced during brain ontogenesis by the Cerebellar and other pioneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layer of the cerebellum. Expression is located in deeper layers in the developing hippocampus and olfactory bulb, low levels of expression are also detected in the immature striatum. At early developmental stages, expressed also in hypothalamic differentiation fields, tectum and spinal cord. A moderate to low level of expression occurs in the septal area, striatal fields, habenular nuclei, some thalamic nuclei, particularly the lateral geniculata, the retina and some nuclei of the reticular formation in the central field of the medulla. Very low levels are found in liver and kidney. No expression in radial glial cells, cortical plate, Purkinje cells and inferior Olivary neurons. The minor isoform 2 is only expressed in non neuronal cells. The minor isoform 3 is found in the same cells as isoform 1, but is almost undetectable in retina and brain stem.

CC -; DEVELOPMENTAL STAGE: First detected at embryonic day 11.5. CC expression increases up to birth and remains high from post-natal day 2 to 11 in both cerebellum and fore/midbrain. Expression decines thereafter and is largely brain specific in the adult.

CC -; DOMAIN: The basic C-terminal region is essential for secretion.

CC -; DISEASE: Defects in reelin are the cause of the autistic recessive reeler (rl) phenotype which is characterized by impaired motor coordination, tremors and ataxia. Neurons in affected mice fail to reach their correct locations in the developing brain, disrupting the organization of the cerebellar and cerebral cortices and other laminated regions.

CC -; SIMILARITY: BELONGS TO THE REELIN FAMILY.

CC -; SIMILARITY: Contains 8 EGF-like domains.

CC -; SIMILARITY: Contains 15 BNR repeats.

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CC EMBL: U24703; AAB31599.1; -; INIT.

DR EMBL; D63520; BAA9788.1; AIR; -INIT.

DR MGD; MGD:103232; Reelin.

DR GO: GO:000742C; P:brain development; IMP.

DR GO; GO:0016477; P:cell migration; IMP.

DR InterPro; IPR002851; IEGF.

DR InterPro; IPR006210; Reeler.

DR Pfam; PF00008; EGF; 5.

DR Pfam; PF02014; Reeler; 1.

DR SMART; SM00181; EGF; 5.

DR PROSITE; PS00022; EGF_1; 7.

DR PROSITE; PS01186; EGF_2; 6.

KW Hydrolase; Serine protease; Developmental protein; Matrix protein; Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal; Alternative splicing; POTENTIAL.

FT SIGNAL 1 26

FT DOMAIN 27 3461 REELIN.

FT DOMAIN 40 172 REELER.

FT DOMAIN 671 762 EGF-LIKE 1.

FT DOMAIN 1030 166 EGF-LIKE 2.

FT DOMAIN 1409 1442 EGF-LIKE 3.

FT DOMAIN 1765 1796 EGF-LIKE 4.

FT DOMAIN 2129 2161 EGF-LIKE 5.

FT DOMAIN 2478 2509 EGF-LIKE 6.

FT DOMAIN 2853 2884 EGF-LIKE 7.

CC Query Match 52.3%; Score 46; DB 1; Length 3461; Best Local Similarity 71.4%; Pred. No. 37; Matches 16; Conservative 0; Missmatches 2; Indels 2; Gaps 1;

Qy 3 YPSGNCLY-YSS 14

Ds 1974 YPGGNIGLYCPYSS 1987

RESULT 6

REIN-RAT STANDARD: PRT; 3462 AA.

AC 258751; ID REIN-RAT; PRT; 3462 AA.

CC 28-FEB-2003 (Rel. 41, Created); DT 28-FEB-2003 (Rel. 41, Last sequence update); DE Reelin precursor (EC 3.4.21.-).

GN Rattus norvegicus (Rat).

RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Sutherida; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]

RC -; SOURCE=cercebellum; (ISOFORM 1).

RN SEQUENCE FROM N.A. (ISOFORM 1).

RA Kikkawa S.; Terashita T.; Submitted (S9EP-2CJC) to the EMBL/GenBank/DB/NC databases.

RN [2]

RP ALTERNATIVE SPlicing.

RP MEDLINE=99263436; PubMed=10326932;

RA Lambert de Rouvroy C.; Bernier B.; Royaux I.; de Sergeyck V.; Goffinet A.M.; RT "Evolutionarily conserved, alternative splicing of reelin: during brain development.", J. Neurol. 156:229-238 (1999).

CC FUNCTION: Extracellular matrix serine protease that plays a role in layering of neurons in the cerebral cortex and cerebellum. Regulates microtubule function in neurons and neuronal migration. Affects migration of sympathetic preganglionic neurons in the spinal cord where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors VLDLR and ApoE2 induces tyrosine phosphorylation of Dab1 and modulation of Tau phosphorylation (By similarity).

CC -; SUBUNIT: Binds to the ectodomains of VLDLR and ApoE2 By similarity.

CC -; SUBCELLULAR LOCATION: Secreted (By similarity).

CC -; ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1; IsoId=P58751-1; Sequence=Displayed;

CC Name=2; IsoId=P58751-2; Sequence=VSP_0C5579;

CC Name=3; IsoId=P58751-3; Sequence=VSP_C05580;

CC -; TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis by the Cajal-Retzius cells and other pioneer neurons located in the telencephalic marginal zone and by granule cells of the external granular layer of the cerebellum.

CC -; DOMAIN: The basic C-terminal region is essential for secretion (By similarity).

CC -; SIMILARITY: BELONGS TO THE REELIN FAMILY.

CC -; SIMILARITY: Contains 8 EGF-like domains.

CC -; SIMILARITY: Contains 15 BNR repeats.

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Mammalia; Butheria; Primates; Catarrhini; Homiridae; Homoc. CC NCBI_TAXID=9606;

RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC TISSUE=Testis;

RX PubMed=12907070;

RA Miyagawa Y., Tanaka H., Iguchi N., Kitamura K., Nakamura Y., Takahashi T., Yamamoto K., Okuyama A., Nishimune Y.; Molecular cloning and characterization of the human orthologue of male germ cell-specific actin capping protein alpha3 (capalpha3). " RT NoJ. Hum. Reprod. 8:531-539(2002). [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Kawakami B., Sugiyama A., Takenoto M., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morimoto M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T., Sugano S.; NEDO human cDNA sequencing project."; Submitted (OCT-2001) to the ENSEMBL/GenBank/CDSB databases. [3]

RN SEQUENCE FROM N.A.

EC TISSUE=Testis;

RX MEDLINE=22288257; PubMed=i2477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altschul S.F., Collins F.S., Wagner J., Schermer C.M., Schuler G.D., Kaushner R.D., Collberg B., Buetow K.H., Schadefer C.F., Bhat N.K., Zeberg B., Moore T., Max S.I., Wang J., Hsien P., Hopkins R.F., Jezdan H., Farmer A.A., Rubin G.M., Hong J., Diatchenko L., Marusina K., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Scaplehorn M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Peers G.J., Loqueland J., Jsdin T.B., Testiynki S., Carrasco P., Prange C., Brownstein M.J., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Bosak S.A., McEwan P.J., McKerron K.J., Abramson R.J., Miltzky S.J., Richards S., Notley K.C., Haie S., Garcia A.M., Gay L.Y., Hulyk S.W., Vialatou D.K., Mizry D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Rodriguez A.C., Grimes J.W., Touchman J.W., Dickson M.C., Butterfield Y.S.N., Krzywinski M.Z., Skalska J., Smajus J.E., Schnerch A., Schein J.E., Jones S.C.M., Marra M.A.; Human and mouse cDNA sequences"; RT Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END; THEREBY BLOCKING THE EXCHANGE OF SUBUNITS AT THESE ENDS); THESE OTHER CAPPING PROTEINS (SUCH AS GELSCIN AND SEVERIN). THESE PROTEINS DO NOT SEVER ACTIN FILAMENTS (BY SIMILARITY).

CC -!- FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END; THEREBY BLOCKING THE EXCHANGE OF SUBUNITS AT THESE ENDS). UNLIKE OTHER CAPPING PROTEINS (SUCH AS GELSCIN AND SEVERIN), THESE PROTEINS DO NOT SEVER ACTIN FILAMENTS (BY SIMILARITY).

CC -!- SUBUNIT: HETEROCHTETRramer OF AN ALPHA AND A BETA SUBUNIT (BY SIMILARITY).

CC -!- TISSUE SPECIFICITY: Expressed exclusively in testis and sperm. Highest expression is found in the neck region of ejaculated sperm with lower levels found in the tail and postacrosome regions.

CC -!- SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT FAMILY.

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CC -!- ENMBL: ABC53259; BAB61501; -

DR ENMBL: AK058174; BAB7103; -

DR ENBL: BC016745; AAH16745; -

DR InterPro: IPR00289; F-actin_capping_A; -

DR Pfam: PF01267; F-actin_capping_A; -

DR PRINTS: PR00191; FACTINCAPA; -

DR ProDom: PD006960; F-actin_cap_A; 1.

DR PROSITE: PS00748; F-ACTIN_CAPPING_A_1; FALSE_NEG.

DR PROSITE: PS00749; F-ACTIN_CAPPING_A_2; -

KW Actin-binding; Capping protein; Multigene family.

PT CONFLICT: 95 95 D->Y (IN REF. 3)

SQ SEQUENCE 299 AA.; 35024 MW.; CEE130C8F1397F67 CRC64;

Query Match Score: 43; DB 1; Length: 299; Best Local Similarity: 60.0%; Pred. No.: 9.3; Matches: 6; Conservative: 6; MisMatches: 3; Indels: 0; Gaps: 0;

Qy 1 DRYPSGNGL 10

nt 131 DHYPKGNCNM 140

RESULT 9

CAZ3_MOUSE

ID CAZ3_MOUSE STANDARD

AC P70150; Q9DN3;

DT 16-OCT-2001 (Rel. 4.0, Created)

DT 15-SEP-2003 (Rel. 4.2, Last annotation update)

DE F-actin capping protein alpha-3 subunit (CapZ alpha-3); (Germ ce1)-specific protein [1].

GN CAPA3 OR GSG3.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bitheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID=10090;

CX RN

SEQUENCE FROM N.A.

STRAIN=573/L6; TISSUE=Testis;

PX MEDLINE=95C46376; PubMed=957958;

RA Taraka H., Yoshimura Y., Nishihara Y., Nozaki M., Nojima H., Nishimura Y.; Yasunaga T., Nishimura Y.; Yasunaga T., Nishimura Y.; "Genomic analysis and characterization of cDNA clones specifically expressed in testicular germ cells." FEBS Lett. 355:41-46(1994).

RL RN

SEQUENCE FROM N.A.

STRAIN=573/L6; TISSUE=Testis;

PX MEDLINE=95C46376; PubMed=957958;

RA Yoshimura Y., Tanaka H., Nozaki M., Yomogida K., Shimamura K., RT "Isolation and characterization of male germ cell-specific actin capping protein alpha." FEBS Lett. 355:193-199(1994).

RL RN

SEQUENCE FROM N.A.

STRAIN=573/L6; TISSUE=Testis;

PX MEDLINE=95C46376; PubMed=957958;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Gaasterland T., Pilai R., Portius J.U., Qi D., Ramchandran S., Kikido I., Osato N., Saito R., Suzuki H., Miyazawa T., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobozi T., Baldarelli R., Hall D.P., Bult C., Hume D.A., Quackenbush J., Schmid L.M., Kanapkin I.V., Matsuda H., Batalov S., Beisel K.W., Blaize J.A., Bradt D., Brusic V., Chothia C., Corban L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer C., Godzik A., Gough J., Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.E., Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Magiotti D.R., Maltsev A., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavian W.J., Perete G., Pescle G., Petruzzello N., Pilai R., Portius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M., Saudek C., Schneider C., Semple C.A., Setou M., Shirada K., Saltana R., Tokesza Y., Taylor M.S., Teasdale C.D., Tomita M., Verardo R., Wagner L., Wanless C., Wells C., Wilring L.G., Wyshaw-Boris A., Yang J., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer P., Hayatsu N., Hirzmann-Kishikawa T., Konno H., Nakamura M., Sakakame N., Sato K., Stirraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Eukuda S.,

RA Hara A., Hashizume W., Ishii K., McKernan K., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers C.,
 RA Birney E., Hayashitaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,773 full-length cDNAs";
 RT Nature 420:563-573 (2002).
 RL [4]

RP SEQUENCE FROM N.A.
 RC TISSUE TESTICLE;
 PX MEDLINE=2238257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Ait schul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Diatchenko L., Jordao H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Stapleton M., Soares V.B., Marusina K., Farmer A.A., Rubin G.N., Hong L.,
 RA Brownstein M.J., Soares V.B., Donaldson M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Logeallano N.A., Peters G.J., Carrinchi P., Prange C.,
 RA Bosak S.A., McEvlan P.J., McKernan K.C., Abramson R.D., Mullaly S.J.,
 RA Richard S., Hale S., Garcia J.A., Ma-Dk J.A., Gunaratne P.H.,
 RA Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pichey J., Helton E., Ketteman M., Yordan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
 RA Schneirach A., Schein J.E., Jones S.C.M., Marras M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human,
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC --: FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT
 CC MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END),
 CC THEREBY BLOCKING THE EXCHANGE OF SUBUNITS AT THESE ENDS. UNLIKE
 CC OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE
 CC PROTEINS DO NOT SEVER ACTIN FILAMENTS. MAY PLAY A ROLE IN THE
 CC MORPHOGENESIS OF SPERMATOZOID.

CC --: SIMILARITY: HETERO-DIMER OF AN ALPHA AND A BETA SUBUNIT (BY
 CC SUBUNIT).

CC --: TISSUE-SPECIFICITY: Exclusively expressed in the testis.

CC --: DEVELOPMENT-STAGE: EXPRESSED IN 24-DAY-OLD AND ADULT TESTIS, BUT
 CC NOT IN 4-, 10- AND 16-DAY-OLD TESTIS.

CC --: SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
 CC FAMILY.

CC --: SIMILARITY: HETERO-DIMER OF AN ALPHA AND A BETA SUBUNIT (BY
 CC SUBUNIT).

CC --: TISSUE-SPECIFICITY: Exclusively expressed in the testis.

CC --: DEVELOPMENT-STAGE: EXPRESSED IN 24-DAY-OLD AND ADULT TESTIS, BUT
 CC NOT IN 4-, 10- AND 16-DAY-OLD TESTIS.

CC --: SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
 CC FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC --: EMBL: D87471; BAA13469.1; -;
 DR NGD: MGI:1062221; Capa3.
 DR PRIM: PFC1367; F-actin_capA; 1.
 DR PRODOM: PDD06950; F-actin_capA; 1.
 DR PROSITE: PS00748; F-actin_cappingA2; 1.
 DR DR PROSITE: PS00749; F-actin_cappingA2; 1.
 DR KW Actin-binding; Capping protein; MuFigene family.
 FT CONFLICT: 117 117 L->I (IN REF. 3).
 FT CONFLICT: 225 225 F->Y (IN REF. 3).
 SQ SEQUENCE 299 AA: 34952 MW: 8C8749313F233C6 CRC64;

Query Match Score: 43; DB: 1; Length: 299;
 Best Local Similarity: 48.9%;
 Matches 6; Conservative 2; Mismatches 0; Gaps 0;

Oy 1 DRYPSGNCGL 10
 Db :31 DHYPNGNCNV 140

RESULT 10
 CA32-RAT STANDARD;
 IC CA23-RAT STANDARD;
 AC Q3WJ76;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE F-actin capping protein alpha-3 subunit (Capz alpha-3).
 GK CAPZA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.
 LN [1];
 OX NCBI_TaxID:10116;
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98069272; PubMed=9406198;
 RA Hurst S.; Howes E.A.; Coadwell J.; Jones R.;
 RT Expression of a testis-specific putative actin-capping protein
 associated with the developing acrosome during rat spermiogenesis.;
 RL Mol. Reprod. Dev. 49:81-91(1998).
 CC --: FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT
 CC MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END)
 CC THEREBY BLOCKING THE EXCHANGE OF SUBUNITS AT THESE ENDS. UNLIKE
 CC OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE
 CC PROTEINS DO NOT SEVER ACTIN FILAMENTS. MAY PLAY A ROLE IN THE
 CC MORPHOGENESIS OF SPERMATOZOID.
 CC --: SIMILARITY: HETERO-DIMER OF AN ALPHA AND A BETA SUBUNIT (BY
 CC SUBUNIT).

CC --: TISSUE-SPECIFICITY: Exclusively expressed in the testis.

CC --: SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
 CC FAMILY.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC --: EMBL: Y12538; CA73137.1; -;
 DR InterPro: IPR00189; F-actin_cap_A.
 DR Pfam: PF01267; F-actin_cap_A; 1.
 DR PRINTS: PRO00191; FACTNCP.
 DR PRODOM: PDD06960; F-actin_capA; 1.
 DR PROSITE: PSC0748; F-actin_cappingA2; 1.
 DR PROSITE: PSC0749; F-actin_cappingA2; 1.
 DR Action-binding; Capping_protein; MuFigene family.
 KW SEQUENCE 299 AA: 35C07 MW: 3D53068BCF79BES CRC64;

Query Match Score: 43; DB: 1; Length: 299;
 Best Local Similarity: 60.0%;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 11
 CHA9 LYMD1 STANDARD;
 AC P50603;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT Chorion class A proteins :D9 (Fragment).

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; AP000C63; BAAB1089_1;
 CC DR; A72513; A72513;
 CC DR; PIR; IPR002830; carboxylyase.
 CC DR; PF01377; UDP_D; 1.
 CC DR; TIGR00148; TIGR00148; i.
 CC DR; Hypothetical protein; Complete proteome,
 CC SEQUENCE; 437 AA; 47635 MN; 505514C80A2D602 CRC64;
 CC KW
 CC SEQUENCE FROM N.A.
 RX MEDLINE=5018300; PubMed=7922786;
 RA Leclerc R.F., Regier J.C.;
 RT "Evolution of chorio: Gene families in lepidoptera: characterization
 of 15 cDNA from the gypsy moth.";
 RL J. Mol. Evol. 39:244-254(1996);
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE
 GYPSY MOTH.
 CC -!- SIMILARITY: MEMBER OF THE ALPHA-BRANCH OF CHORION PROTEIN TO WHICH
 BELONGS CLASSES A, CA AND HCA.

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 or send an email to license@isb-sib.ch).

CC -----
 CC DR; JG661; AAA65861_1; -
 KW EGGSHELL; Chorion; Repeat; Multigene family.
 FT NON_TER 1
 SC SEQUENCE 121 AA; 11617 MN; 528E28501E205617 CRC64;
 CC -----
 Query Match 46.6%; Score 41; DB 1; Length: 21;
 Best Local Similarity 66.7%; Pred. No. 78;
 Yatches 6; Conservative 2; Mismatches 1; Indels 3; Gaps 0;
 RN 2 RYPSGNGL 1C
 QY | | : | : ;
 Db 4: RYPAGACGI 49
 CC -----
 YK78_AERPE STANDARD; PRT; 437 AA.
 ID 09Y650;
 AC DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical protein APB2078.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
 OC Desulfurococcaceae; Aeropyrum.
 OC NCB; TaxID=56636;
 RN 1; -
 RP SEQUENCE FROM N.A.
 RC STRAIN=KI_12;
 RX PubMed=10382966;
 FA Kawarabayashi Y., Horikawa H., Yamazaki S., Hatai K., Hatai A., Kosugi H.,
 RA Jin-no K., Takahashi M., Sekine K., Baba S.-I., Nishizawa K., Nakazawa H.,
 RA Hosoyama Y., Fukui S., Nagai Y., Nishizawa K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funabashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki S., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 crenarchaeon, Aeropyrum pernix K1.";
 RT Res. 6:83-101(1999).
 RL CC -----
 CC -!- SIMILARITY: Belongs to the ubid family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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SM Protein - Protein search, using sw model

RUN ID: November 5, 2003, 16:37:23 ; Search time: 38236 seconds

(without alignments;
1952.598 Million cell updates/sec)

Title: US-09-902-563-18

Perfect score: 88

Sequence: -DYPYSSNCGLYSSG 15

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 630525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_atheia:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_hexameric:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_micr:*
- 8: sp_organell:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rhodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_viru:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	88	100.0	357	11	Q9EPT7	Q9ept7; rattus norv
2	88	ICJ.0	442	6	Q8MIP7	Q8mip7 sus scrofa
3	56	63.6	220	5	Q7BA2	Q7ba2 ciona savie
4	56	63.6	652	5	Q9NDQ1	Q9ndq1 ciona intestinalis
5	46	52.3	1785	4	Q9Y211	Q9y211 homo sapien
6	46	52.3	1785	4	Q9Y4V9	Q9y4v9 homo sapien
7	46	52.3	2403	4	Q9UGY2	Q9ugy2 homo sapien
8	46	52.3	2412	4	Q9UJ57	Q9uj57 homo sapien
9	46	52.3	2413	4	Q9EDD4	Q9edd4 homo sapien
10	46	52.3	2413	4	Q9UKJ4	Q9ukj4 homo sapien
11	46	52.3	2426	4	Q9UGY3	Q9ugy3 homo sapien
12	51.1	183	4	Q8TAE0	Q8tae0 homo sapien	
13	45	51.1	210	4	Q8NBS2	Q8nbs2 homo sapien
14	45	51.1	210	4	Q8TAC6	Q8tac6 homo sapien
15	45	50.6	457	11	Q8R0Z6	Q8r0z6 mus musculus
16	44	50.0	217	7	Q9GJH7	Q9gjh7 salmo trutta

RESULT 1

29EPT7 PRELIMINARY; PRT; 357 AA.

ID Q9EPT7; AC Q9EPT7;

DT 01-MAR-2001 (TREMBL); 16, Created;

DT 01-MAR-2001 (TREMBL); 16, Last sequence update;

DT 31-DEC-2001 (TREMBL); 19, Last annotation update)

DE Prothrombinase FGL2.

DS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Nematalia; Suthoria; Scutognathida; Muridae; Murinae; Rattus.

CX CX_1 TAXID:101;

RN SEQUENCE FROM K.A.

RC Rychlik D.F.; Chien E.; Philippe M.; Phillippe Rat";

RC "FGL2 Expression in the Sprague-Dawley Rat";

DR Submitted (AUG-2001) to the BMSJ/GenBank/EBI databases.

DR EMBL: AF2323608; ARAG2269.1; -;

DR ISSN: PC2671; LFZD;

DR INTERPRO: IPE002181; Fibrinogen_C.

DR PLAM: PFC0147; Fibrinogen_C; 1.

DR SMART: SM00186; FBG; 1.

DR PROSITE: PS00541; FBGRIN_AGC_DCMAIN; 1.

DR SEQPILE: 357 AA; 40966 MW;

DR DRYPGNCNGLYSSG 15

DR ||||| ||||| |||||

DR DRYPGNCNGLYSSG 296

DR 282

PRT; 442 AA.

ID Q8MIP7;

AC Q8MIP7;

DT 01-OCT-2002 (TREMBrel. 22; Created)
 DT 01-OCT-2002 (TREMBrel. 22; Last sequence update)
 DT CI-MAR-2003 (TREMBrel. 23; Last annotation update)

DE Fibrinogen-like protein.
 GN CI-FBRN.
 OS Ciona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phleobranchia; Cionidae; Ciona.
 NCBI_TaxID=7719;
 RN [1];
 RP SEQUENCE FROM N.A.
 RA Hotta K.; Takahashi H.; Asakura T.; Saitoh Y.; Takatori N.; Satou Y.;
 RA Satoch N.;
 RT "Characterization of Brachyury downstream notochord genes in the Ciona
 intestinalis embryo";
 RT submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AB012657; BAB00636.1; -;
 DR HSSP; P02671; IF2D;
 DR InterPro; IPR002181; Fibrinogen_C.
 DR PF0147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRNAGC_DOMAIN; 1.
 DR PROSITE; FS00C514; FIBRNAGC_DOMAIN; 1.
 SQ SEQUENCE 442 AA; 50575 MW; -67800D67AEFF899 CRC64;
 GQ Query Match 100.0%; Score 88; DB 6; Length 442;
 Best Local Similarity 100.0%; Pred. No. 2.6e-36; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DRB 1 DRYPSGNCGLYYSSG 15
 DRB 367 DRYPSGNCGLYYSSG 381

RESULT 3
 Q8TBAAZ PRELIMINARY; PRT; 220 AA.
 AC Q8TBAAZ
 DT 01-JUN-2002 (TREMBrel. 21; Created);
 DT 01-JUN-2002 (TREMBrel. 21; Last sequence update);
 DT 01-OCT-2002 (TREMBrel. 22; Last annotation update);
 DE Fibrinogen-like protein (Fragment).
 CS FIBRIN-LIKE
 OS Ciona savignyi.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phleobranchia; Cionidae; Ciona.
 NCBI_TaxID=51511;
 RN [1];
 RP SEQUENCE FROM N.A.
 MEDLINE=1920613; PubMed=11923238;
 RA Imai K.S.; Satoch N.; Satou Y.;
 RT "Early embryonic expression of FGF4/5/9 gene and its role in the
 induction of mesendoderm and notochord in Ciona savignyi embryos."
 RL Development; 129:1729-1738 (2002).
 EMBL; AB073373; BAB88674; 1; -;
 InterPro; IPR002181; Fibrinogen_C.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRNAGC_DOMAIN; 1.
 PR NONTER 1 1 220 AA; 25758 MW; 4160FAE72F3EDG6 CRC64;
 SQ SEQUENCE 220 AA; 25758 MW; 4160FAE72F3EDG6 CRC64;
 GQ Query Match 63.6%; Score 56; DB 5; Length 220;
 Best Local Similarity 66.7%; Pred. No. 3.24; Mismatches 5; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 DRB 2 DRYPSGNCGLYYSSG 15
 DRB 143 DGYALGNCGYYRSSG 157

RESULT 5
 Q8Y2A1 PRELIMINARY; PRT; 1785 AA.
 AC Q8Y2A1
 DT 01-NOV-1993 (TREMBrel. 12; Created);
 DT 01-NOV-1993 (TREMBrel. 12; Last sequence update);
 DT 01-MAR-2003 (TREMBrel. 23; Last annotation update);
 DE DMBT1.
 GN DMbt1.
 CS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1];
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2001778; PubMed=10551316;
 RA Takeshita H.; Sato M.; Shibusaki H.O.; Sembra S.; Sakurada A.; Hoshi M.;
 RA Hayashi Y.; Tagawa Y.; Ayabe H.; Horii A.;
 RT "Expression of the DMbt1 gene is frequently suppressed in human lung
 cancer";
 RL Jpn. J. Cancer Res. 90:903-908 (1999);
 RC 1-SIMILARITY: BAAT8577.1;
 DR EMBL; AB020851; BAAT8577.1; JOINED.
 DR EMBL; AB020812; BAAT8577.1; JOINED.
 DR EMBL; AB020813; BAAT8577.1; JOINED.
 DR EMBL; AB020814; BAAT8577.1; JOINED.
 DR EMBL; AB020815; BAAT8577.1; JOINED.
 DR EMBL; AB020816; BAAT8577.1; JOINED.
 DR EMBL; ABC020817; BAAT8577.1; JOINED.
 DR EMBL; ABC020818; BAAT8577.1; JOINED.
 DR EMBL; ABC020819; BAAT8577.1; JOINED.
 DR EMBL; AB020820; BAAT8577.1; JOINED.
 DR EMBL; AB020822; BAAT8577.1; JOINED.
 DR EMBL; ABC020823; BAAT8577.1; JOINED.
 DR EMBL; AB020824; BAAT8577.1; JOINED.
 DR EMBL; AB020825; BAAT8577.1; JOINED.
 DR EMBL; ABC020826; BAAT8577.1; JOINED.
 DR EMBL; AB020827; BAAT8577.1; JOINED.
 DR EMBL; AB020829; BAAT8577.1; JOINED.
 DR EMBL; AB020830; BAAT8577.1; JOINED.
 DR EMBL; AB020831; BAAT8577.1; JOINED.

RESULT 4
 Q9NDQ1 PRELIMINARY;
 AC Q9NDQ1
 DT 01-OCT-2000 (TREMBrel. 15; Created);
 DT 01-OCT-2000 (TREMBrel. 15; Last sequence update);
 DT 01-DEC-2001 (TREMBrel. 19; Last annotation update)

RESULT 8			
ID Q9U557	PRELIMINARY;	PRT; 2412 AA.	
AC Q9U557;			
DT 01-MAY-2000	(TREMBLeL 13, Created)		
DT 01-MAR-2003	(TREMBLeL 19, Last sequence update)		
GN DMBT1.	DMBT1/8kb.2 protein precursor.		
OS Homo sapiens (Human)			
OC Xukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarhini; Homidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FRCM N.A.			
RC MEDLINE=9415538; PubMcD=104B53C5;			
RX Holmskov J., Mollerhaeue J., Maden J., Vitved J., Granelund J., Torre L., Klem A., Reid K.B., Pousska A., Skoeld K.; "Cloning of gp-3340, a putative opsonin receptor for lung surfactant protein E"; Proc. Natl. Acad. Sci. U.S.A. 96:10794-10799 (1999).			
CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.			
DR EMBL; AJ243212; CAB56155.1;			
DR HSSP; P29392; 1SFPP.	CUB domain.		
DR InterPro; IPR000855.	Endoglin/CD105.		
DR InterPro; IPR001507.	Intein.		
DR InterPro; IPR001141.	Srcr_receptor.		
DR Pfam; PF00431; CUB_2.			
DR Pfam; PF00356; SRCR_1.			
DR SMART; SM00042; SFERACTRCPTR.			
DR SMART; SM00042; CUB_2.			
DR SMART; SM000202; SR_14.			
DR SMART; SM00241; ZPA_1.			
DR TIGRFAMS; TIGR01443; Intein_Cterm.	13.		
DR PROSITE; PS01100; CUB_2.			
DR PROSITE; PS00420; SRCR_1.	13.		
DR PROSITE; PS50087; SRCR_2.	14.		
DR PROSITE; PS00682; ZP_DOMAIN_1.			
KN Signal.			
FT CHAIN	26	2413 AA;	PROTEIN.
FT SIGNAL	1	25	DMBT1/8KB_2
FT SEQUENCE	2413 AA;	260600 MW;	PROTEIN.
Qy 4 PSGNCG-LYSSG 15			99A449CSF4F60728 CRC64;
Qy 4 PSGNCG-LYSSG 15			Score 46; DB 4; Length 2413;
Qy 4 PSGNCG-LYSSG 15			Best Local Similarity 52.3%; Score 46; DB 4; Length 2413;
Qy 4 PSGNCG-LYSSG 15			Matches 9; Conservative 9; Similarity 64.3%; Prd. No. 1.3e+02; Indels 2; Gaps 1;
Db :762 PSSNCGGFLFYASG 1775			Matches 9; Conservative 9; Similarity 64.3%; Prd. No. 1.3e+02; Indels 2; Gaps 1;
RESULT 10			
ID Q9UK4	PRELIMINARY;	PRT; 2413 AA.	
AC Q9UK4;			
DT 01-MAY-2000	(TREMBLeL 13, Created)		
DT 01-MAR-2003	(TREMBLeL 13, Last sequence update)		
GN SP-340.	variant protein.		
OS Homo sapiens (Human)			
CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
DR MEDLINE=9415938; PubMed=10495905;			
DR InterPro; IPR000859; CUB domain.			
DR InterPro; IPR001507; Endoglin/CD105.			
DR InterPro; IPR006144; Intein.			
DR InterPro; IPR001100; Srcr_receptor.			
DR Pfam; PF00431; CUB_2.			
DR Pfam; PF0050; SRCR_1.			
DR Prints; PR0028; SFERACTRCPTR.			
DR SMART; SM00042; SR_14.			
DR SMART; SM00241; ZPA_1.			
DR TIGR01443; Intein_Cterm.	14.		
DR PROSITE; PS01180; CUB_2.			
DR PROSITE; PS00420; SRCR_1.			
DR PROSITE; PS50087; SRCR_2.			
DR PROSITE; PS00682; ZP_DOMAIN_1.			
KN Signal.			
FT CHAIN	26	2412 DMBT1/8KB_2 PROTEIN.	PROTEIN.
FT SEQUENCE	2412 AA;	260568 MW;	PROTEIN.
Qy 4 PSGNCG-LYSSG 15			Score 46; DB 4; Length 2412;
Qy 4 PSGNCG-LYSSG 15			Best Local Similarity 52.3%; Score 46; DB 4; Length 2412;
Qy 4 PSGNCG-LYSSG 15			Matches 9; Conservative 9; Mismatches 2; Indels 2; Gaps 1;
Db :762 PSSNCGGFLFYASG 1775			Matches 9; Conservative 9; Mismatches 2; Indels 2; Gaps 1;
RESULT 9			
ID Q96DU4	PRELIMINARY;	PRT; 2413 AA.	
AC Q96DU4;			
DT 01-DEC-2001	(TREMBLeL 19, Created)		
DT 01-DEC-2001	(TREMBLeL 19, Last sequence update)		
GN DMBT1.	DMBT1/8kb.2 protein precursor.		
OS Homo sapiens (Human)			
CC Xukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC Mammalia; Eutheria; Primates; Catarhini; Homidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TIGR01443; Intein_Cterm.	14.		
DR TIGR01443; Intein_Cterm.	14.		
DR PROSITE; PS01180; CUB_2.			
DR PROSITE; PS00420; SRCR_1.			
DR PROSITE; PS50087; SRCR_2.			
DR PROSITE; PS00682; ZP_DOMAIN_1.			
KN Signal.			
FT CHAIN	26	2412 AA;	PROTEIN.
FT SEQUENCE	2412 AA;	260568 MW;	PROTEIN.
Qy 4 PSGNCG-LYSSG 15			Score 46; DB 4; Length 2412;
Qy 4 PSGNCG-LYSSG 15			Best Local Similarity 52.3%; Score 46; DB 4; Length 2412;
Qy 4 PSGNCG-LYSSG 15			Matches 9; Conservative 9; Mismatches 2; Indels 2; Gaps 1;
Db :762 PSSNCGGFLFYASG 1775			Matches 9; Conservative 9; Mismatches 2; Indels 2; Gaps 1;

RC TISSUE=Lymph node;
 RA Li R., Han H., Wang J.;
 RT "RBP, a novel protein interacting with LIN protein Kct7.";
 RL Submitted [MAR-2002] to the EMBL/GenBank/DDBJ databases.
 [2]
 RN
 SEQUENCE FROM N.A.

RP TISSUE=Kidney;

RA Strausberg R.;

RL Submitted [JUN-2002] to the EMBL/GenBank/DDBJ databases.

DR EMBL: AF493783; AAM12662.1; -;

DR EMBL: AF493786; AAM12665.1; -;

DR EMBL: BC03096; AAH3096.1; -;

SQ SEQUENCE 21C AA: 23114 MW: FCCAAFI166C37967 CRC64;

Query Match Score 45; DB 4; Length 21C;
 Best Local Similarity 51.1%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 YPSNCGLYSS 14

Db 95 YTSQQGKYYSS 106

RESULT 15

QBR026 ID QBR026 PRELIMINARY; PROT; 457 AA.

AC QBR026;

DT 01-JUN-2002 (TREMBrel 21; Created;

DR 01-JUN-2002 (TREMBrel 21; Last sequence update)

DE 01-MAR-2003 (TREMBrel 23; Last annotation update)

DE Similar to angiopoietin-related protein 5 (AKP3).

GN 63040B1Rik CR ARP3.

OS Mus musculus (Mouse);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Xantharia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.

CX NCBI_TaxID:10090;

EN [1]

SEQUENCE FROM N.A.

RP TISSUE=Liver;

RA Strausberg R.;

RL Submitted [MAR-2002] to the EMBL/GenBank/DDBJ databases.

[2]
 RN

RP TISSUE FROM N.A.

RA Matsushita S., Saito Y., Masuho Y., Yasunaga K., Cike Y., Suda T.;

RL Submitted [JAN-2001] to the EMBL/GenBank/DDBJ databases.

[3]
 RN

SEQUENCE FROM N.A.

RA Oike Y., Suda T.;

RT "Molecular cloning of ARP3."

RL Submitted [MAY-2002] to the EMBL/GenBank/DDBJ databases.

DR EMBL: BC025904; AAH25904.1; -;

DR MGD: MGI:1917976; 6330404E1Rik.

DR InterPro: IPK002101; Fibrinogen_C.

DR Pfam: PF00147; fibrinogen_C.

DR PROSITE: PS03514; FIBRN_NG_C_DOMAIN_1.

SQ SEQUENCE 457 AA; 5195 MW; BTCA299E3FEC6C3E CRC64;

Query Match Score 50.6%; DB 11; Length 457;
 Best Local Similarity 60.0%; Pred. No. 40;
 Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Oy 1 DRYPSGNCLGLYSSG 15

Db 391 DS-YSGNCALYHRGG 404

Search completed: November 5, 2003, 16:48:00
 Job time : 27.9324 secs

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GW protein - protein search, using sw model

Run on: November 5, 2003, 15:56:26 ; Search time 2.94053 seconds
(without alignments)
6C9.684 Million cells updated/sec

Title: US-09-902-563-18
Perfect score: 88
Scoring table: BiOSTM62

Sequence: 1 DRYPSGNCGYSSG 15
Gapext 0.5
Maximum DB seq length: 20330000000

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:
-1.07863

Post-processing: Maximum Match 0%
Minimum Match 10%
Listing first 45 summaries

Database : A_Geneseq19Jun03;*

- 1: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1980.DAT;*
- 2: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1981.DAT;*
- 3: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1982.DAT;*
- 4: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1983.DAT;*
- 5: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1984.DAT;*
- 6: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1985.DAT;*
- 7: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1986.DAT;*
- 8: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1987.DAT;*
- 9: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1988.DAT;*
- 10: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1989.DAT;*
- 11: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1990.DAT;*
- 12: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1991.DAT;*
- 13: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1992.DAT;*
- 14: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1993.DAT;*
- 15: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1994.DAT;*
- 16: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1995.DAT;*
- 17: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1996.DAT;*
- 18: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1997.DAT;*
- 19: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA1998.DAT;*
- 20: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA2000.DAT;*
- 21: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA2001.DAT;*
- 22: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA2002.DAT;*
- 23: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA2003.DAT;*
- 24: /SIDS1/ggdata/geneseq/geneseqp-emb1/AA2004.DAT;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	89	100.0	15	20	AW88237	Human prothrombin
2	89	100.0	432	20	AW88236	Mouse prothrombin
3	88	100.0	439	20	AW88225	Human prothrombin
4	50	56.8	53	23	ABP34223	Human angiopoietin
5	47	53.4	93	22	AAB3347	Human gene 1 encod
6	46	52.3	102	22	ABG25291	Novel human diagno
7	46	52.3	666	19	AW64590	Human SRGP protein
8	46	52.3	1785	19	AW64591	Human SRGP protein
9	46	52.3	346C	23	ABB05007	Human reelin prote

PR 10-OCT-1997; 97US-0061644.
PR 15-MAY-1997; 97US-0046537.

PD 19-NOV-1998.
PP 15-MAY-1998; 98W0-C000475.
PA {LEVY/; LEVY G.
PA Levy G;
PA Levy G;
XX WPI; 1999-059687/C5.
XX Modulating immune coagulation - by using Fg-2 antibodies and

:0	4.6	52.3	3461	23	ABB05008	Mouse reelin prote
:11	4.6	52.3	3470	22	ABG25.97	Novel human diagno
:13	4.5	51.1	123	22	AAU80079	Acptair: association
:14	4.5	51.1	126	22	AAU80078	Acptair: association
:15	4.5	126	23	AAJ014806	Human apoptin-assoc1:	
:16	4.5	158	21	AAB427516	Apoptin-assoc2:	
:17	4.5	51.1	210	22	AAJ38085	Apoptin-assoc3:
:20	4.5	51.1	210	23	ABP43315	Human cytoskeleton
:21	4.4	50.0	292	22	AAE32106	Human BCa3 protein #1;
:22	4.3	48.9	299	24	AAE32106	Drosophila melanog
:23	4.3	48.9	460	20	AAY34589	Human cytoskeleton
:24	42.5	48.3	193	18	AAW55378	Chlamydia pneumoniae
:25	42.5	48.3	193	23	AAW5013	H. pylori CRP 07cp
:26	42.5	48.3	493	18	AAW5517	Helicobacter pylor
:27	42.5	48.3	493	23	AAW50311	Helicobacter pylor
:28	42.5	48.3	696	18	AAW55618	H. pylori outer me
:29	42.5	48.3	696	20	AAV17207	Helicobacter pylor
:30	42.5	48.3	696	23	AAW50310	Human PRO178 prote
:31	42.5	48.3	696	23	AAW50310	Human NEW angiopo
:32	41.5	47.2	219	24	AAE32250	Human angiopoletin
:33	41.5	47.2	279	22	AAV72626	Human angiopoletin
:34	41.5	47.2	342	22	AAV72626	Human TIE ligand N
:35	41.5	47.2	470	20	AAV03398	Human PRO178 prote
:36	41.5	47.2	470	21	AAB24389	Human NEW angiopo
:37	41.5	47.2	470	22	AAB51330	Human angiopoletin
:38	41.5	47.2	470	22	AAB53066	Human TIE ligand N
:39	41.5	47.2	470	23	ABG80357	Human angiogenesis
:40	41.5	47.2	470	23	ABB95424	Human TIE ligand N
:41	41.5	47.2	470	23	AAE19627	Human PRO178 prote
:42	41.5	47.2	470	23	ABB84418	Callosoga spider ve
:43	41	46.6	39	17	AAWC540	Callosoga spider ve
:44	41	46.6	39	17	AAW05343	Callosoga spider ve
:45	41	46.6	80	17	AAW05343	Callosoga spider ve

ALIGNMENTS

RESUL1	AAW98237	standard: Peptide, 15 AA.
XX	XX	AAW98237:
XX	XX	15-MAR-1999 ;First entry:
XX	XX	Human prothrombinase Fg12 epitope.
XX	XX	Prothrombinase: hfg12; Fg12; human; immune coagulation; antibody; inhibitor; infection; graft; rejection; Glomerulonephritis; cancer; gastrointestinal disease; foetal loss; therapy; vaccine; epitope.
OS	OS	Homo sapiens.
XX	XX	WC9851235-A1.
XX	XX	PD 19-NOV-1998.
PP	PP	15-MAY-1998; 98W0-C000475.
PR	PR	10-OCT-1997; 97US-0061644.
PR	PR	15-MAY-1997; 97US-0046537.
PA	PA	{LEVY/; LEVY G.
PA	PA	Levy G;
PA	PA	Levy G;
XX	XX	Levy G;
DR	DR	WPI; 1999-059687/C5.
XX	XX	Modulating immune coagulation - by using Fg-2 antibodies and
???	???	

PT Compounds, used to treat conditions including graft rejection and foetal loss
 XX
 PS Claim 4; Page 72; 105pp; English.

XX This peptide corresponds to amino acid residues 364-378 of human prothrombinase Fg12 (see AAW80235). A claimed method of preventing or treating a condition requiring a reduction in immune coagulation comprises administering an inhibitor of Fg12. The inhibitor is preferably an antibody that binds to the Fg12 epitope. The condition to be treated in graft rejection or foetal loss (claimed).

XX Sequence 15 AA;

Query Match 100.0%; Score 88; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRYPSGNCGIYSSG 15
 Db 1 DRYPSGNCGIYSSG 15

RESULT 2
 AAW80236 standard; Protein; 432 AA.
 XX
 AAW80236:
 AC
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Mouse prothrombinase Fg12 protein.
 XX
 KW Prothrombinase; Fg12; mouse; immune coagulation; antibody;
 KW inhibitor; infection; graft rejection; glomerulonephritis; cancer;
 KW gastrointestinal disease; foetal loss; therapy; vaccine.
 XX
 NS Mus sp.

XX Key Location/Qualifiers
 PT Modified-site 172..174 Asn is N-glycosylated
 PT Modified-site 228..231 /note= "Asn is N-glycosylated"
 PT Modified-site 256..259 /note= "Asn is N-glycosylated"
 PT Modified-site 323..325 /note= "Asn is N-glycosylated"
 PT Domain 213..439 /note= "fibrinogen related domain"
 PT Peptide 98W0-CAG0475, /note= "epitope (Claim 4;"
 XX WO9851335-A1.
 XX
 PN 19-NCV-1998.
 PD 15-MAY-1998;
 XX 98W0-CAG0475,
 XX 97US-0061684,
 PR 15-OCT-1997;
 PR 15-MAY-1997;
 XX 97US-0046537.
 PA (LEVY /) LEVY G.

XX
 PA (LEVY /) LEVY G.
 P- Levy G;
 XX
 DR WPI: 1999-C59687/05.
 DR N-PSDB; AAV84140.
 XX
 PT Modulating immune coagulation - by using Fg12 antibodies and compounds, used to treat conditions including graft rejection and foetal loss
 XX
 PS Claim 8; Page 70-71; 105pp; English.

XX This is the amino acid sequence of mouse prothrombinase Fg12, as predicted from Fg12 DNA (see AAV84140). Fg12 is a 70 kDa transmembrane serine protease that has immune procoagulant activity. The human Fg12 amino acid sequence is given in AAW80236. The invention provides a method for inhibiting immune coagulation by inhibiting the activity or expression of Fg12. The method can be used in vivo to treat a condition which requires a reduction in immune coagulation such as bacterial and viral infections, cancer, glomerulonephritis, a number of gastrointestinal diseases, allograft and xenograft rejection and foetal loss. An Fg12-specific antibody, an Fg12 antisense oligonucleotide, or a substance that affects prothrombinase activity of a Fg12 protein may be used to treat a condition requiring a reduction in procoagulant activity. A vaccine containing an Fg12 protein or peptide is used for prevention of graft rejection or foetal loss (claimed).

CC This is the amino acid sequence of mouse prothrombinase Fg12, as predicted from Fg12 DNA (see AAV84140). Fg12 is a 70 kDa transmembrane serine protease that has immune procoagulant activity. The human Fg12 amino acid sequence is given in AAW80236. The invention provides a method for inhibiting immune coagulation by inhibiting the activity or expression of Fg12. The method can be used in vivo to treat a condition which requires a reduction in immune coagulation such as bacterial and viral infections, cancer, glomerulonephritis, a number of gastrointestinal diseases, allograft and xenograft rejection and foetal loss. An Fg12-specific antibody, an Fg12 antisense oligonucleotide, or a substance that affects prothrombinase activity of a Fg12 protein may be used to treat a condition requiring a reduction in procoagulant activity. A vaccine containing an Fg12 protein or peptide is used for prevention of graft rejection or foetal loss (claimed).

CC Query Match 100.0%; Score 88; DB 20; Length 432;
 CC Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Sequence 432 AA;

Query 1 DRYPSGNCGIYSSG 15
 Db 357 DRYPSGNCGIYSSG 371

RESULT 3
 AAW80235
 ID AAW80235 standard; Protein; 439 AA.
 XX
 AC AAW80235;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Human prothrombinase Fg12 protein.
 XX
 KW Prothrombinase; Fg12; human; immune coagulation; antibody;
 KW inhibitor; infection; graft rejection; glomerulonephritis; cancer;
 KW gastrointestinal disease; foetal loss; therapy; vaccine.
 XX
 CS Homo sapiens.
 XX
 PT Key Location/Qualifiers
 PT Modified-site 172..174 Asn is N-glycosylated
 PT Modified-site 228..231 /note= "Asn is N-glycosylated"
 PT Modified-site 256..259 /note= "Asn is N-glycosylated"
 PT Modified-site 323..325 /note= "Asn is N-glycosylated"
 PT Domain 213..439 /note= "Asn is N-glycosylated"
 PT Peptide 98W0-CAG0475, /note= "epitope (Claim 4;"
 XX WO9851335-A1.
 XX
 PN 19-NCV-1998.
 PD 15-MAY-1998;
 XX 98W0-CAG0475,
 XX 97US-0061684,
 PR 15-OCT-1997;
 PR 15-MAY-1997;
 XX 97US-0046537.
 PA (LEVY /) LEVY G.

XX
 PA (LEVY /) LEVY G.
 P- Levy G;
 XX
 DR WPI: 1999-C59687/05.
 DR N-PSDB; AAV84140.
 XX
 PT Modulating immune coagulation - by using Fg12 antibodies and compounds, used to treat conditions including graft rejection and foetal loss
 XX
 PS Claim 8; Page 70-71; 105pp; English.

XX Modulating immune coagulation - by using Fg12 antibodies and
 PR compounds, used to treat conditions including graft rejection and
 PT foetal loss.

XX Claim 3: Page 66-67; 105pp; English.

XX This is the amino acid sequence of human prothrombinase Fg12, as
 CC predicted from Fg12 DNA (see AAvg4-39). Fg12 is a 70 kDa
 CC transmembrane serine protease having procoagulant activity.
 CC The invention provides a method for inhibiting immune coagulation by
 CC inhibiting the activity or expression of Fg12. The method can be
 CC used in vivo to treat a condition which requires a reduction in
 CC immune coagulation such as bacterial and viral infections, cancer,
 CC gilomerulonephritis, a number of gastrointestinal diseases,
 CC allograft and xenograft rejection and foetal loss. An Fg12-specific
 CC antibody, an Fg12 antisense oligonucleotide, or a substance that
 CC affects prothrombinase activity of Fg12 protein may be used to
 CC treat a condition requiring a reduction in procoagulant activity.
 CC A vaccine containing an Fg12 protein or peptide is used for
 CC prevention of graft rejection or foetal loss (claimed).

XX Sequence 439 AA:

Query Match Score 100.0%; Length 439;
 Best Local Similarity 100.0%; Pred. No. 3.6E-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Cy 1 DRYPSGNCGLYYSSG 15
 DE 364 DRYPSGNCGLYYSSG 378

RESULT 4

2D ABP34223 standard; Protein: 53 AA.

XX ABP34223;

XX 08-JUL-2002 (first entry)

XX Human angiopoietin-like ORF3196 protein, SEQ ID NC:6392.

XX Human; open reading frame; ORF; drug screening; diagnosis;
 KW disease monitoring; cytokine; cell; proliferation; cell differentiation;
 KW immune modulation; haemostasis regulation; tissue growth;
 KW angiogenesis; activation; inhibition; chemotactic; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; pulmonary;
 KW viscoelastic; antipsoriatic; antidiabetic; cytostatic; nootropic;
 KW neuroprotective; antithrombotic; anticoagulant; thromolytic;
 KW cardiotonic; hypotensive; antithyroid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; viricide; antibacterial; fungicide.

XX Homo sapiens.

XX WO200190366-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2C01WO-US17076.

XX 24-MAY-2000; 20CCUS-206690P.

XX (CURA-) CURAGEN CORP.

XX Beach MD, Shimkets RA;

XX WPI; 2002-106200/14.

DR N-PSDB; ABN78249.

XX Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation -

XX PS Claim 10; Page 1846; 2508PP; English.

XX Sequences ABP31028-ABP3551 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-CC 75054 represent cDNAs encompassing them. The invention also encompasses CC ABN7387 representing cDNAs encoding them. The invention also encompasses CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the CRFX polynucleotides, vectors and host cells comprising CRFX polynucleotides, the recombinant production of CRFX proteins, antibodies specific for CRFX proteins, methods of detecting CRFX polynucleotides and polypeptides, methods of screening for modulators of CRFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The CRFX proteins of the invention have a wide range of biological activities, such as cytotoxic, cell proliferation, cell differentiation, immune modulation, haemostasis regulation, chemotactic, chemokinetic activity, haemostatic activity, thrombolytic activity, chemokine receptor/ligand, antiinflammatory activity, tumor inhibition activity, and antiinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behavior. CRFX proteins, nucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and Alzheimer's disease, neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. CRFX nucleic acids may also be used as a source of primers and probes, in the detection of CRFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The CRFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of CRFX protein, and in drug screening. The CRFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of CRFX-associated diseases.

XX Sequence 53 AA:

Query Mat: Score 50; DB 23; Length 53;
 Best Local Similarity 66.7%; Pred. No. 2.4;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PSGNCGLYYSSG 15
 Db 20 PSGNCALYHRGG 3;

RESULT 5

ABE3342
 2D ABE3347 standard; peptide: 93 AA.

XX ABE3341;

XX 10-AUG-2001 (first entry)

XX Human; gene 1 encoded secreted protein fragment, SEQ ID NC:122.
 KW secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; hematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; alligraphy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angina; pregnancy-related disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; urinary;

KW Cell culture; chemotaxis; food additive; gene therapy;
KW binding partner identification.

XX ABG25291
ID ABG25291 standard; protein; 102 AA.
XX ABG25291;
XX AC
XX DT 18-FEB-2002 (first entry)
XX Novel human diagnostic protein #25282.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX CS
XX PD 17-NAY-2001.
XX PN WO200134800-A1.
XX 2D
XX 2F 08-NOV-2003; 2003WO-US30674.
XX PR 12-NOV-1995; 99US-0164750.
XX PR 30-JUN-2003; 2000US-0215128.
XX PA (HUMA-) HUMAN GENOME SCI. INC.
XX PI Ruben SM, Komatsu GA, Ebner R, Fisselai M, Wei F;
XX DR 1293085/34.
XX WPI; 2001-1293085/34.
XX New nucleic acid molecules encoding human secreted proteins used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers -
XX Disclosure, Page 501; 530pp; English.
CC AAD0705-AAD07759 represent cDNAs corresponding to 19 human secreted
CC proteins genes, and AAE0392-AAE03346 represent the proteins they encode.
CC AAE03347-AAE03375 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of one new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 29 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proinvasive disorders, cancer, tumours, focal and developmental
CC abnormalities, haematoepicietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurologcal disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy related disorders, endocrine
CC disorders, and infectious diseases. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties
CC antibiotics specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC immunoassay (ELISA). The present sequence represents a human
CC secreted protein fragment referred to in the disclosure of the invention.
XX Sequence 93 AA;

Query Match 53.4%; Score 47; DB 22; Length 93;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Cg 4 PSGNCGLYSSG 15
Db 32 PSENANCALYQRGGG 43

Query Match 52.3%; Score 46; DB 22; Length 102;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
Cg 3 YPS3NCGLY-YSS 14
Db 86 YPG3NIGLYCPSS 99

RESULT 7
AAW64590
ID AAW64590 standard; Protein; 666 AA.

RESULT 6
AAW64590

WPI; 2002-096596/13.
 DR N-PSDB; ABA92604.
 Novel composition useful for screening compounds that modulate Reelin binding to low density lipoprotein receptor, comprising an isolated Reelin polypeptide and low density lipoprotein receptor -
 PT XX
 PS XX
 Claim 16; Column 31-48; 45pp; English.

XX The present invention describes a composition (I) comprising an isolated reelin protein (II) bound to an isolated low density lipoprotein receptor (LDLR) (III). (II) is an extracellular glycoprotein of approximately 385 kDa containing a small region of similarity with F-spondin at the N terminus, a stretch of positively charged amino acids at the C terminus, and a series of eight internal repeats of 350-390 amino acids, each repeat containing two related sub-domains that flank a pattern of conserved cysteine residues known as an epidermal growth factor (EGF)-like motif. (I) has neuroprotective, nocrotropic and anti-lipaemic activities, and can be used as a modulator of reelin-LDLR interaction. (I) is useful in screen for compounds that modulate reelin binding to an LDLR, in an assay system, where the assay system comprises a microplate array and an automated robotic microprocessor controlled system for adding and removing reagents to the microplate array. The compounds identified by the above screening method are useful as therapeutic agents to provide or alleviate a diverse spectrum of diseases including neurodegenerative disorders such as Alzheimer's disease, to facilitate neuronal regeneration after injury, to prevent or alleviate lipid metabolism diseases, to enhance cognitive functions and memory or to ameliorate other developmental disorders. The present sequence represents mouse (Mus musculus) reelin, which is used in the exemplification of the present invention.

XX Sequence 3460 AA;

Query Match 52.3%; Score 46; DB 23; Length 3460;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02;
 Matches 10; Conservative 0; N mismatches 2; Gaps 1;

Cy 3 YFSGNGLY-YSS 14
 Db 1973 YPGGNIGLYCPSS 1987

RESULT 1.0
 ABB5338
 ID ABB5008 standard; Protein: 3461 AA.
 XX
 AC AB3C5008;
 XX DT 21-MAR-2002 (first entry);
 DE XX
 DE Mouse reelin protein SEQ ID NO: 2.
 XX
 KW Mouse; reelin; low density lipoprotein receptor; LDLR; neuroprotective;
 KW extracellular glycoprotein; nocrotropic; anti-lipaemic; Alzheimer's disease;
 KW neurodegenerative disorder; neuronal regeneration; cognitive function;
 KW lipid metabolism disease; memory; developmental disorder.
 XX
 CS Mus muscius.
 XX
 PN JS6323177-B1.
 XX
 PD 27-NOV-2001.
 XX
 PF 16-JUN-1999; 99US-0334220.
 XX
 PR 16-JUN-1999; 99US-0334220.

PA (S)JUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 XX
 PI Curran T, D'Arcangelo G;
 XX
 DR WPI; 2002-096596/13.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring

DR N-PSDB; ABA92603.
 XX Novel composition useful for screening compounds that modulate Reelin binding to low density lipoprotein receptor, comprising an isolated Reelin polypeptide and low density lipoprotein receptor -
 PT XX
 PS XX
 Claim 16; Column 47-64; 45pp; English.

XX The present invention describes a composition (I) comprising an isolated reelin protein (II) bound to an isolated low density lipoprotein receptor (LDLR) (III). (II) is an extracellular glycoprotein of approximately 385 kDa containing a small region of similarity with F-spondin at the N terminus, a stretch of positively charged amino acids at the C terminus, and a series of eight internal repeats of 350-390 amino acids, each repeat containing two related sub-domains that flank a pattern of conserved cysteine residues known as an epidermal growth factor (EGF)-like motif. (I) has neuroprotective, nocrotropic and anti-lipaemic activities, and can be used as a modulator of reelin-LDLR interaction. (I) is useful in screen for compounds that modulate reelin binding to an LDLR, in an assay system, where the assay system comprises a microplate array and an automated robotic microprocessor controlled system for adding and removing reagents to the microplate array. The compounds identified by the above screening method are useful as therapeutic agents to provide or alleviate a diverse spectrum of diseases including neurodegenerative disorders such as Alzheimer's disease, to facilitate neuronal regeneration after injury, to prevent or alleviate lipid metabolism diseases, to enhance cognitive functions and memory or to ameliorate other developmental disorders. The present sequence represents mouse (Mus musculus) reelin, which is used in the exemplification of the present invention.

Sequence 3461 AA;
 Query Match 52.3%; Score 46; DB 23; Length 3461;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02;
 Matches 10; Conservative 0; N mismatches 2; Gaps 1;
 PT 3 YFSGNGLY-YSS 14
 DC 1974 YPGGNIGLYCPSS 1987

RESULT 1.1
 ABB57265
 ID ABB57265 standard; Protein: 3461 AA.
 XX
 AC ABB57265;
 XX DT 27-MAR-2002 (first entry);
 DE XX
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:129.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasoconstrictor ischaemia; ischaemic condition; ischaemic disease.
 XX
 OS Mus musculus.
 PN WO200188188-A2.
 XX
 PD 22-MAY-2001.
 XX
 PF 16-MAY-2001; 2001WO-JP04192.
 PR 18-MAY-2000; 2000JP-0145977.
 XX
 PA (UNIV NIPPON SCHOOL JURIDICAL PERSON.
 XX
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX
 DR WPI; 2002-034733/04.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring

PT expression levels of particular genes defined in the specification or
 PT by determining the expression profile of a gene group comprising these
 PT genes -
 XX Claim 2; Page 385-400; 2690pp; English.

CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vascular ischaemia) by measuring
 CC expression levels of particular genes (AB9922C2 to AB9929-2, encoding
 CC the protein sequences in A83570C to ABB5374); or by determining the
 CC expression profile of a gene group comprising these genes. The
 CC genes are used as an indicator when screening for ischaemic condition-improving
 CC drugs or therapeutic agents for ischaemic diseases. ABI9923 and ABI9924
 CC represent PCR primers for a mouse ischaemic condition related sequence,
 CC which are used in the exemplification of the present invention.

XX Sequence 3462 AA;
 SQ Query Match: 52.3%; Score: 46; DB: 23; Length: 3461;
 Best Local Similarity 21.4%; Pred. No. 6.4e+02;
 Matches 1C; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 3 YPSGNGLY--YSS 14
 Db 1974 YPGGNIGLYCPYSS 1987

RESULT 12
 AB925297 ID AB925297 standard; Protein: 3470 AA.
 XX AC AAU80679;
 XX DT 30-JUL-2002 (first entry)

XX Novel human diagnostic protein #252288.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder;
 KW Homo sapiens.
 EN WO200175067-A2.
 XX FC 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2002; 2002US-C540217.
 PR 23-AUG-2006; 2000US-3649167.
 XX PA (HYSE-) HYSEQ INC.

XX Dumanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 DR N-P5DB; AAS89484.

XX New isolated polynucleotide and encoded polypeptides, useful in:
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID NO 565656; 203pp; English.
 XX WPI: 2001-639362/73.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (III). The
 CC poly nucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (III) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (III) and its binding partners are useful in medical
 CC imaging or sites expressing (III). (I) and (II) are useful for creating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABGC0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://www.wipo.int/pub/published_pct_sequences.

SQ Sequence 3470 AA;

Query Match: 52.3%; Score: 46; DB: 22; Length: 3470;
 Best Local Similarity 71.4%; Pred. No. 6.4e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 3 YPSGNGLY--YSS 14
 Db 1983 YPGGNIGLYCPYSS 1996

RESULT 13
 AAU80679 ID AAU80679 standard; Protein: 123 AA.
 XX AC AAU80679;
 XX DT 30-JUL-2002 (first entry)

XX Apoptin-associating protein 5 (AAP-5), partial sequence.
 DE Cancer; PACT; cytostatic; immunosuppressive; AAP-5;
 KW Apoptin-associating protein 5; p53-independent apoptosis;
 KW cei- proliferation; cell death; autoimmune disease.
 XX Homo sapiens.
 OS XX EPI138768-A2.
 PN XX PD 04-OCT-2001.
 XX FF 27-YAR-2001; 2001EP-0201137.
 XX PR 27-YAR-2000; 2000EP-0201108.
 XX PA LEAD: LEADD BV.
 XX PI Noteborn XHM, Roth CJL, Darren-van Oorschot AAAM,
 XX DR NPI: 2001-657960/76.
 XX PT New apoptin-associating protein 5 for inducing p53-independent
 PT apoptosis, or for treating cancer or autoimmune disease -
 XX Disclosure: Page 23; 44pp; English.

CC The invention relates to an isolated or recombinant nucleic acid
 CC which encodes an apoptin-associating protein 5 (AAP-5) capable of
 CC providing apoptosis, or its functional fragment. The nucleic acid, a
 CC vector comprising the nucleic acid, or a pharmaceutical composition
 CC useful for the induction of p53-independent apoptosis. The pharmaceutical
 CC composition comprising the nucleic acid, vector comprising the nucleic
 CC acid or the pharmaceutical substance is also useful for the induction of
 CC p53-independent apoptosis, or for the treatment of a disease where

CC enhanced cell proliferation or decreased cell death; is observed, such as
 CC cancer, or autoimmune disease. The present sequence represents the
 CC partial amino acid sequence of apoptin-associating protein 5 (AAP-5).
 XX SQ sequence 123 AA;

Query Match Score 45; DB 22; Length :23;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 14
 AAJ80778 Standard; Protein: 126 AA.
 XX
 ID AAU800778
 AC AAU800778;
 XX
 DT 30-JUL-2002 (first entry)
 DE Apoptin-associating protein 5 (AAP-5).
 XX Cancer; pACT; cytostatic; immunosuppressive; AAP-5;
 KW Apoptin-associating protein 5; p53-independent apoptosis;
 KW Cell proliferation; cell death; autoimmune disease.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 PH Region 1..3
 PT /note= "Encoded by PACT vector"
 XX EP1138768-A2.
 XX PD 04-CCT-2C01.
 XX PF 27-MAR-2001; 2001EP-0201137.
 XX PR 27-MAR-2000; 2000EP-0201138.
 XX PA (LEAD); LEADD BV.
 XX PI Noteborn MM, Rohn JL, Danen-van Cortscht AAM;
 XX DR 2001-657960/76.
 XX N-PSDB; AB650949.
 XX PT New apoptin-associating protein 5 for inducing p53-independent
 PT apoptosis, or for treating cancer or autoimmune disease. -
 XX Claim 1C; Fig 2; 44pp; English:
 PS The invention relates to an isolated or recombinant nucleic acid
 XX which encodes an apoptin-associating protein 5 (AAP-5) capable of
 CC providing apoptosis, or its functional fragment. The nucleic acid,
 CC vector comprising the nucleic acid, or a proteinaceous substance is
 CC useful for the induction of p53-independent apoptosis. The pharmaceutical
 CC composition comprising the nucleic acid, vector comprising the nucleic
 CC acid or the proteinaceous substance is also useful for the induction of
 CC p53-independent apoptosis, or for the treatment of a disease where
 CC enhanced cell proliferation or decreased cell death is observed, such as
 CC cancer or autoimmune disease. The present sequence represents the
 CC amino acid sequence of apoptin-associating protein 5 (AAP-5).
 XX SQ Sequence 126 AA;

Query Match Score 45; DB 23; Length 126;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YPSGNCGLYSS 14
 DD :||| |||
 11 YTSSQCGRYYSS 22

RESULT 15
 AAC14806
 ID AAO14806 standard; Protein: 126 AA.
 XX
 AC AAO14806;
 XX DT 06-JUL-2002 (first entry)
 DE Human apcptin-associating protein 5, with pACT expression vector region.
 XX Human; PACT expression vector; apoptin-associating protein 5; AAP-5;
 KW AAP-6; p53-independent apoptosis; gene therapy; cancer;
 KW autoimmune disease; apoptosis pathway cascade.
 XX
 CS Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 PT Peptide 1..3
 PT /note= "This region is derived from the multiple cloning
 site in the pACT expression vector"
 PT Protein 4..126
 PT /note= "This region represents the human apoptin-
 associating protein 5 (AAP-5)"
 XX EP1138768-A1.
 XX PR 04-OCT-2C01.
 XX PF 27-MAR-2C00; 2000EP-02C01108.
 XX PR 27-MAR-2C00; 2000EP-0201108.
 XX PA (LEAD); LEADD BV.
 XX Noteborn MM, Rohn JL, Danen-van Cortscht AAM;
 XX DR 2002-012523/C2.
 XX N-PSDB; AAL42576.
 XX WPI; 2002-012523/C2.
 XX New Proteins useful for inducing p53-independent apoptosis and for
 PT treating cancer and autoimmune diseases comprises the isolated or
 PT recombinant apoptin-associating proteinaceous substance -
 XX Disclosure; Fig 3; 23pp; English:
 XX The invention comprises the amino acid and coding sequences of two
 CC apoptin-associating proteins (AAP-5 and AAP-6) and
 CC protein sequences are useful for inducing p53-independent apoptosis, and
 CC the diagnosis/treatment (gene therapy) of cancer and autoimmune diseases.
 CC The AAP-5/AAP-6 DNA and protein sequences are also useful for finding
 CC additional apoptin-associating proteinaceous substances from the
 CC apoptosis pathway cascade. The present amino acid sequence represents the
 CC human AAP-5 protein (with a region derived from the multiple cloning
 CC site of the pACT expression vector).
 XX Sequence 126 AA;

Query Match Score 45; DB 23; Length 126;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YPSGNCGLYSS 14
 DD :||| |||
 11 YTSSQCGRYYSS 22

Search completed: November 5, 2003, 16:46:00

Wed Nov 5 17:46:54 2003

us-09-902-563-18.rag

Page 9

Job time : 3.94051 secs

		%	SUMMARIES			
		Query Match	Length	DB ID	Description	
1:	/cgn2_6/_picodata/2/_pubpaa/us07	PUBCOMB.pep:**				
2:	/cgn2_6/_picodata/2/_pubpaa/us07_pc**	NEW_PUB.pep:**				
3:	/cgn2_6/_picodata/2/_pubpaa/us06	NEW_PUB.pep:**				
4:	/cgn2_6/_picodata/2/_pubpaa/us06_pc**	PUBCOMB.pep:**				
5:	/cgn2_6/_picodata/2/_pubpaa/us07_pc**	NEW_PUB.pep:**				
6:	/cgn2_6/_picodata/2/_pubpaa/_petus_pc**	PUBCOMB.pep:**				
7:	/cgn2_6/_picodata/2/_pubpaa/us08_new	FJB.pep:**				
8:	/cgn2_6/_picodata/2/_pubpaa/us08_pc**	PUBCOMB.pep:**				
9:	/cgn2_6/_picodata/2/_pubpaa/us09a	PUBCOMB.pep:**				
10:	/cgn2_6/_picodata/2/_pubpaa/us09b	PUBCOMB.pep:**				
11:	/cgn2_6/_picodata/2/_pubpaa/us09c	PUBCOMB.pep:**				
12:	/cgn2_6/_picodata/2/_pubpaa/us09_new	PUBCOMB.pep:**				
13:	/cgn2_6/_picodata/2/_pubpaa/us10a	PUBCOMB.pep:**				
14:	/cgn2_6/_picodata/2/_pubpaa/us103	PUBCOMB.pep:**				
15:	/cgn2_6/_picodata/2/_pubpaa/us10c	PUBCOMB.pep:**				
16:	/cgn2_6/_picodata/2/_pubpaa/us10_new	PUB.pep:**				
17:	/cgn2_6/_picodata/2/_pubpaa/us60_new	FJB.pep:**				
18:	/cgn2_6/_picodata/2/_pubpaa/us60_pc**	PUBCOMB.pep:**				

Pre: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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Query Match      30.0%; Score 88; DB 11; Length 15;
Best Local Similarity 30.0%; Pred. Nc. 4.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy   1 DRPSGNCGLYSSG 15
      ||||||| | | | | |
Dt   1 DRPSGRGCGLYSSG 15

```

RESULT 2
US-1C-096-255-18
Sequence 18, Application US/10696255
Publication No. US20030103974A1
GENERAL INFORMATION:
APPLICANT: Levy, Gary
APPLICANT: Clark, David A.
TITLE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 957-52

CURRENT APPLICATION NUMBER: US/10/096,255
 CURRENT FILING DATE: 2002-03-13
 PRIOR APPLICATION NUMBER: US 60/346,537
 PRIOR FILING DATE: 1997-05-17
 PRIOR APPLICATION NUMBER: US 60/061,684
 PRIOR FILING DATE: 1997-10-10
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 18
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 3
 US-10-096-255-4
 Query Match 100.0%; Score 88; DB 15; Length 432;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DRYPSGNCGLYSSG 15
 Db 357 DRYPSGNCGLYSSG 371

RESULT 5
 US-09-902-563-2
 Sequence 2, Application US/09902563
 Publication No. US20030099654A1
 GENERAL INFORMATION:
 APPLICANT: Levy, Gary
 TITLE OF INVENTION: Methods of Modulating Immune Coagulation
 FILE REFERENCE: 9579-37
 CURRENT APPLICATION NUMBER: US/09/902,563
 CURRENT FILING DATE: 2002-08-09
 PRIOR APPLICATION NUMBER: US 09/442,143
 PRIOR FILING DATE: 1999-11-15
 NUMBER OF SEQ ID NOS: 53
 SEQ ID NO: 2
 LENGTH: 439
 TYPE: PRT
 ORGANISM: Homo sapiens fg12

RESULT 6
 US-10-096-255-2
 Sequence 2, Application US/10096255
 Publication No. US2003C103974A1
 GENERAL INFORMATION:
 APPLICANT: Clark, David A.
 TITLE OF INVENTION: Methods of Modulating Immune Coagulation
 FILE REFERENCE: 9579-52
 CURRENT APPLICATION NUMBER: US/10/096,255
 CURRENT FILING DATE: 2002-03-13
 PRIOR APPLICATION NUMBER: US 09/442,143
 PRIOR FILING DATE: 1999-11-15
 NUMBER OF SEQ ID NOS: 53
 SEQ ID NO: 2
 LENGTH: 439
 TYPE: PRT
 ORGANISM: Homo sapiens fg12

RESULT 4
 US-10-096-255-4
 Sequence 4, Application US/10096255
 Publication No. US2003010397A1
 GENERAL INFORMATION:
 APPLICANT: Levy, Gary
 APPLICANT: Clark, David A.
 TITLE OF INVENTION: Methods of Modulating Immune Coagulation
 FILE REFERENCE: 9579-52
 CURRENT APPLICATION NUMBER: US/10/096,255
 CURRENT FILING DATE: 2002-03-13
 PRIOR APPLICATION NUMBER: US 60/046,537
 PRIOR FILING DATE: 1997-05-17
 PRIOR APPLICATION NUMBER: US 60/061,684
 PRIOR FILING DATE: 1997-10-10
 NUMBER OF SEQ ID NOS: 53
 SEQ ID NO: 4
 LENGTH: 432
 TYPE: PRT
 ORGANISM: Murine fg12

RESULT 7
 US-10-096-255-5
 Sequence 5, Application US/09902563
 Publication No. US20030099654A1
 GENERAL INFORMATION:
 APPLICANT: Levy, Gary
 TITLE OF INVENTION: Methods of Modulating Immune Coagulation
 FILE REFERENCE: 9579-37
 CURRENT APPLICATION NUMBER: US/09/902,563
 CURRENT FILING DATE: 2002-08-09
 PRIOR APPLICATION NUMBER: US 09/442,143
 PRIOR FILING DATE: 1999-11-15
 NUMBER OF SEQ ID NOS: 53
 SEQ ID NO: 2
 LENGTH: 439
 TYPE: PRT
 ORGANISM: Murine fg12

US-09-819-308-2
 ; Sequence 2, Application US/09819308
 ; Patent No. US20020019042A1
 ; GENERAL INFORMATION:
 ; APPLICANT: No. US20020019042A1 Leborn, Mathieu
 ; APPLICANT: Danoen-van Oorschot, Astrid
 ; APPLICANT: Roijn, Jennifer
 ; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
 ; FILE REFERENCE: 2906-4820US
 ; CURRENT APPLICATION NUMBER: US/09/819,308
 ; CURRENT FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 ; LENGTH: 126
 ; TYPE: PRT
 ; ORGANISM: vector pMT2SM-AAP-5

US-09-819-308-2
 Query Match 5: 1%; Score 45; DB 9; Length 126;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 4; Indels 0;
 Gaps 0;
 Qy 3 YPSGNGLYSS 14
 Db 11 YTSSQGKYYSS 22

RESULT 8
 US-09-819-308-1C
 ; Sequence 10, Application US/C9819308
 ; Patent No. US20019040A1
 ; GENERAL INFORMATION:
 ; APPLICANT: No. US20020019040A1 Leborn, Mathieu
 ; APPLICANT: Danoen-van Oorschot, Astrid
 ; APPLICANT: Roijn, Jennifer
 ; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
 ; FILE REFERENCE: 2906-4820US
 ; CURRENT FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn version 3.0
 SEQ ID NO 10
 ; LENGTH: 210
 ; TYPE: PRT
 ; ORGANISM: Open reading frame of AAP-5

US-09-819-308-10
 Query Match 5: 1%; Score 45; DB 9; Length 210;
 Best Local Similarity 66.7%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 4; Indels 0;
 Gaps 0;
 Qy 3 YPSGNGLYSS 14
 Db 95 YTSSQGKYYSS 106

RESULT 9
 US-09-832-355A-24
 ; Sequence 24, Application US/C9832355A
 ; Publication No. US2003027751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kessier, Paul
 ; TITLE OF INVENTION: VSG FUSION PROTEINS
 ; FILE REFERENCE: 205654
 ; CURRENT APPLICATION NUMBER: US/09/812,355A
 ; CURRENT FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 126
 ; SOFTWARE: PatentIn version 3.0
 SEQ ID NO 24
 ; LENGTH: 219
 ; TYPE: PRT

Query Match 1%; Score 41.5; DB 11; Length 219;
 Best Local Similarity 60.0%; Pred. No. 93;
 Matches 9; Conservative 0; Mismatches 5; Indels 1;
 Gaps 1;
 Qy 1 DRYPSGNGLYSSG 15
 Db 153 DSY-SGNCALYQRGG 166

RESULT 1C
 US-11-394-557-6
 ; Sequence 6, Application US/11394557
 ; Publication No. US200317529A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Godowski, Paul J.
 ; Gurney, Austin L.
 ; TITLE OF INVENTION: Tie Ligands
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 YEDIUM TYPE: 3.5 inch, 1.44 Mc floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DCS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 FILING DATE: 21-Mar-2003
 APPLICATION NUMBER: US/10/394,557
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 FILING DATE: 19-SEPT-1997
 APPLICATION NUMBER: US/08/933,821
 REGISTRATION NUMBER: 33,055
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: P1130
 TELEPHONE: 650/225-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 470 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-11-394-557-6

Query Match 1%; Score 41.5; DB 12; Length 473;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indels 1;
 Gaps 1;

Query Match 1%; Score 41.5; DB 12; Length 473;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indels 1;
 Gaps 1;

RESULT 11
 US-1C-223-081-4
 ; Sequence 4, Application US/10223081
 ; Publication No. US2003036866A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Marsters, Scot A.
 APPLICANT: Pan, James
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Ye, Weilan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
 FILE REFERENCE: P3235P1C3
 CURRENT APPLICATION NUMBER: US 10/223,082
 CURRENT FILING DATE: 2002-08-16
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: US 10/081,056
 PRIOR APPLICATION NUMBER: US 60/213,637
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 60/220,664
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: US 60/222,695
 PRIOR FILING DATE: 2000-08-02
 PRIOR APPLICATION NUMBER: US 09/643,657
 PRIOR FILING DATE: 2000-08-17
 PRIOR APPLICATION NUMBER: PCT/US00/23522
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: PCT/US00/23328
 PRIOR FILING DATE: 2000-08-24
 Remaining Prior Application data removed - See File Wrapper or PAML.
 NUMBER OF SEQ ID NOS: 383

SEQ ID NO 4

Query Match Score 41.5%; DB 12; Length 470;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indexis 1; Gaps 1;

27 1 DRYPSGNCGLYSSG 15
 Db 434 DSY-SGNCAlyCrgg 417

RESULT 13
 US 10/223-085-4

Query Match Score 41.5%; DB 12; Length 470;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indexis 1; Gaps 1;

27 1 DRYPSGNCGLYSSG 15
 Db 434 DSY-SGNCAlyCrgg 417

RESULT 14
 US 10/223-082-4

GENERAL INFORMATION:
 Publication No. US20030130497A1
 APPLICANT: Baker, Kevin P.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Marsters, Scot A.
 APPLICANT: Pan, James
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Williams, P. Mickey

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
 FILE REFERENCE: P3235P1C10
 CURRENT APPLICATION NUMBER: US 10/223,085
 CURRENT FILING DATE: 2002-08-16
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: US 60/213,637
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 60/219,556
 PRIOR FILING DATE: 2000-07-20
 PRIOR APPLICATION NUMBER: US 60/220,624
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: US 09/643,657
 PRIOR FILING DATE: 2000-08-17
 PRIOR APPLICATION NUMBER: PCT/US00/23522
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: PCT/US00/23328
 PRIOR FILING DATE: 2000-08-24
 Remaining Prior Application data removed - See File Wrapper or PAML.
 NUMBER OF SEQ ID NOS: 383

SEQ ID NO 4

Query Match Score 41.5%; DB 12; Length 470;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indexis 1; Gaps 1;

27 1 DRYPSGNCGLYSSG 15
 Db 434 DSY-SGNCAlyCrgg 417

RESULT 15
 US 10/223-085-4

Query Match Score 41.5%; DB 12; Length 470;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indexis 1; Gaps 1;

27 1 DRYPSGNCGLYSSG 15
 Db 434 DSY-SGNCAlyCrgg 417

RESULT 16
 US 10/223-082-4

GENERAL INFORMATION:
 Publication No. US20030191059A1
 APPLICANT: Baker, Kevin P.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Marsters, Scot A.
 APPLICANT: Pan, James
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Williams, P. Mickey

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
 FILE REFERENCE: P3235P1C10
 CURRENT APPLICATION NUMBER: US 10/223,085
 CURRENT FILING DATE: 2002-08-16
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: US 60/213,637
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 60/219,556
 PRIOR FILING DATE: 2000-07-20
 PRIOR APPLICATION NUMBER: US 60/220,624
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: US 09/643,657
 PRIOR FILING DATE: 2000-08-17
 PRIOR APPLICATION NUMBER: PCT/US00/23522
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: PCT/US00/23328
 PRIOR FILING DATE: 2000-08-24
 Remaining Prior Application data removed - See File Wrapper or PAML.
 NUMBER OF SEQ ID NOS: 383

SEQ ID NO 4

Query Match Score 41.5%; DB 12; Length 470;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indexis 1; Gaps 1;

27 1 DRYPSGNCGLYSSG 15
 Db 434 DSY-SGNCAlyCrgg 417

RESULT 17
 US 10/223-082-4

GENERAL INFORMATION:
 Publication No. US20030191059A1
 APPLICANT: Baker, Kevin P.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Marsters, Scot A.
 APPLICANT: Pan, James
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Williams, P. Mickey

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
 FILE REFERENCE: P3235P1C10
 CURRENT APPLICATION NUMBER: US 10/223,085
 CURRENT FILING DATE: 2002-08-16
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: US 60/213,637
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 60/219,556
 PRIOR FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/22C, 624
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: US 60/22C, 664
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: PCT/US03/20710
 PRIOR FILING DATE: 2000-07-08
 PRIOR APPLICATION NUMBER: US 60/222, 695
 PRIOR FILING DATE: 2000-08-02
 PRIOR APPLICATION NUMBER: US 09/643, 657
 PRIOR FILING DATE: 2000-08-17
 PRIOR APPLICATION NUMBER: PCT/US03/23522
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: PCT/US03/23328
 PRIOR FILING DATE: 2000-08-24
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 383
 SEQ ID NO 4
 LENGTH: 470
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-223-C84-4

Query Match Score 41.5; DB 15; Length: 470;
 Best Local Similarity 60.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 5; Insertions 1;
 Gaps 1;

Qy 1 DRYPSGNCGJYYSSG 15
 Db 404 DSY-SGNCA-LYCRGG 417

RESULT 15
 US-10-223-C88-4
 Sequence 4 Application US/10223098
 Publication No. US2003010501A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Marsers, Scot A.
 APPLICANT: Par, James
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Watanae, Colin K.

APPLICANT: Wood, William I.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Ye, Weilan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
 FILE REFERENCE: P3235PICE
 CURRENT APPLICATION NUMBER: US/10/223, 088
 CURRENT FILING DATE: 2002-08-16
 PRIOR APPLICATION NUMBER: US 10/081, 056
 PRIOR FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: US 60/213, 637
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 60/219, 556
 PRIOR FILING DATE: 2000-07-20
 PRIOR APPLICATION NUMBER: US 63/220, 624
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: US 60/220, 664
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: PCT/US00/2070
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: US 60/222, 695
 PRIOR FILING DATE: 2000-08-02
 PRIOR APPLICATION NUMBER: US 09/643, 657
 PRIOR FILING DATE: 2000-08-17
 PRIOR APPLICATION NUMBER: PCT/US00/23522
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: PCT/US03/23328
 PRIOR FILING DATE: 2000-08-24
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 383
 SEQ ID NO 4
 LENGTH: 470
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-223-088-4

Wed Nov 5 17:46:55 2003

usb-09-902-563-18.rapb

Page 6

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Best Local Similarity 60.0%; Pred. No. 2e+02; Mismatches 5; Indels 2; Caps 1;
Matches 9; Conservative 0; MisMatches 5; Indels 2; Caps 1;

Qy      1 DRYPSGNCGIYSSG 15
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Db      404 DSY-SGRCALYORG 417
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Job time : 1.68302 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode:

Run on: November 5, 2003, 16:44:23 ; Search time 1.35727 Seconds
(without alignments)
603.285 Million cell updates/sec

Title: US-C3-902-563-18

Perfect score: 88

Sequence: 1 DRYPSGNGLYSSG 15

Scoring table: BLOSUM62

Gapcost 10.0 ; Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_MA_*

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2: /cgn2_6/prodata/1/iaa/5B-COMB pep:*
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4: /cgn2_6/ptodata/1/iaa/6B-COMB pep:*
5: /cgn2_6/prodata/1/iaa/PCUTS-COMB pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	88	100.0	432	US-09-442-143A-16
2	88	100.0	439	US-09-442-143A-4
3	88	100.0	439	US-09-442-143A-2
4	46	52.3	676	US-09-341-587-1
5	46	52.3	1785	US-09-341-587-3
6	46	52.3	3460	US-09-34-220-1
7	46	3461	4	US-09-34-220-2
8	43	48.9	160	US-09-34-432A-7
9	42	47.7	409	US-09-328-352-6858
10	41.5	47.2	470	US-08-943-82-6
11	41.5	47.2	470	US-08-960-507-6
12	41.5	47.2	470	US-C9-336-828-6
13	41.5	47.2	470	US-09-342-92A-6
14	41.5	47.2	470	US-09-346-801-6
15	41.5	47.2	470	US-09-332-928-6
16	41.5	47.2	470	US-09-333-075-6
17	41.5	47.2	470	US-09-203-08A-6
18	41.5	47.2	470	US-09-333-077-6
19	41.5	46.6	39	US-08-390-88A-1
20	41	46.6	39	US-08-390-68A-2
21	40	45.5	1041	US-08-494-74A-2
22	40	45.5	1245	PCT-JS96-1C12-2
23	39.5	44.9	99	US-08-537-4C0-19
24	39.5	44.9	212	US-09-106-568E-15G
25	39.5	44.9	139	US-09-451-47C-9
26	39	44.3	38	US-08-390-882A-3
27	39	44.3	39	US-08-390-882A-3

ALIGNMENTS

RESULT 1
US-09-442-143A-18
Sequence 18, Application US/09442-43A
Patent No. 6403089
GENERAL INFORMATION:
APPLICANT: Levy, Gary A.
TITLE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442-143A
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: US 60/046,537
PRIOR FILING DATE: 1997-05-17
PRIOR APPLICATION NUMBER: 1997-10-10
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO: 15
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
JS-09-442-143A-18

Query Match Similarity 100.0%; Score 88; DB 4; Length 15;
Best Local Matches 15; Conservativeness 0; Mismatches 0; Indels 0;
Gaps 0;
QY : - DRYPSGNGLYSSG 15
Dy : 1 DRYPSGNGLYSSG 15
RESULT 2
US-09-442-143A-4
Sequence 4, Application US/09442143A
Patent No. 6403089
GENERAL INFORMATION:
APPLICANT: Levy, Gary A.
TITLE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442-143A
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: US 60/046,537
PRIOR FILING DATE: 1997-05-17
PRIOR APPLICATION NUMBER: 1997-10-10
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO: 4

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LENGTH: 432
TYPE: PRT
ORGANISM: Murine fg12
S-09-442-143A-4

RESULT 5
US-09-341-587-3
Query Match 100.0%; Score 88; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.2e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Del 0;
SEQ ID NO: 1 DRYPSGNCGLYYSSG 15
357 DRYPSGNCGLYYSSG 371

RESULT 3
US-09-442-143A-2
Sequence 2, Application US/09442-43A
Patent No. 64C3089

GENERAL INFORMATION:
APPLICANT: Clair, David A.
TITLE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442,43A
PRIORITY FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: US 60/046,537
PRIOR FILING DATE: 1997-05-17
PRIOR APPLICATION NUMBER: US 60/061,684
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NCS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NC: 2
LENGTH: 439
TYPE: PRT
ORGANISM: Homo sapiens fg12
S-09-442-143A-2

Query Match 100.0%; Score 88; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.2e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Del 0;
SEQ ID NO: 1 DRYPSGNCGLYYSSG 15
364 DRYPSGNCGLYYSSG 378

RESULT 4
US-09-341-587-2
Sequence 1, Application US/09341-587
Patent No. 6346606

GENERAL INFORMATION:
APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-1CA
CURRENT APPLICATION NUMBER: US/C9/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-39
NUMBER OF SEQ ID NCS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 1
LENGTH: 666
TYPE: PRT
ORGANISM: Homo sapiens
S-09-341-587-1

Query Match 52.3%; Score 46; DB 4; Length 666;
Best Local Similarity 64.3%; Pred. No. 36; Indels 2; Gaps 2;
Matches 9; Conservative 2; Mismatches 1; Del 1;
SEQ ID NO: 1
4 PSGNCG-LYYSSG 15
183 PSSNCGFLYASG 196

RESULT 5
US-09-341-587-3
Sequence 3, Application US/C9341587
Patent No. 6346606
GENERAL INFORMATION:
APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-10
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
NUMBER OF SEQ ID NCS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 3
LENGTH: 1785
TYPE: PRT
ORGANISM: Homo sapiens
US-09-341-587-3

Query Match 52.3%; Score 46; DB 4; Length 1785;
Best Local Similarity 64.3%; Pred. No. 98; Indels 2; Gaps 1;
Matches 9; Conservative 2; Mismatches 1; Del 1;
Qy 4 PSGNCG-LYYSSG 15
Dc 1134 PSSNCGFLYASG 1147

RESULT 6
US-09-341-220-1
Sequence 1, Application US/C933422C
Patent No. 6123177

GENERAL INFORMATION:
APPLICANT: St. Jude Children's Research Hospital
APPLICANT: Curran, Thomas
APPLICANT: D'Arcangelo, Gabriella
TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND THERAPY
FILE REFERENCE: 242270F734
CURRENT APPLICATION NUMBER: US/69/334,220
CURRENT FILING DATE: 1999-06-16
NUMBER OF SEQ ID NCS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NC: 1
LENGTH: 3460
TYPE: PRT
ORGANISM: Homo sapien
US-09-341-220-1

Query Match 52.3%; Score 46; DB 4; Length 3460;
Best Local Similarity 71.4%; Pred. No. 1.9e-02; Indels 2; Gaps 1;
Matches 10; Conservative 3; Mismatches 2; Del 1;
Qy 3 YPSGNCGLY-YSS 14
Dc 1973 YPGNIGLYCPSS 1986

RESULT 7
US-C9-334-220-2
Sequence 2, Application US/09334220
Patent No. 6343277

GENERAL INFORMATION:
APPLICANT: St. Jude Children's Research Hospital
APPLICANT: Curran, Thomas
APPLICANT: D'Arcangelo, Gabriella
TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND THERAPY
FILE REFERENCE: 242270F734
CURRENT APPLICATION NUMBER: US/69/334,220
CURRENT FILING DATE: 1999-06-16
NUMBER OF SEQ ID NCS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NC: 1
LENGTH: 3460
TYPE: PRT
ORGANISM: Homo sapien
US-C9-334-220-2

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FILE REFERENCE: 2427/0F704
 CURRENT APPLICATION NUMBER: US/09/334,220
 CURRENT FILING DATE: 1999-06-16
 NUMBER OF SEQ ID NCS: 5
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NC 2
 LENGTH: 3461
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-334-220-2

Query Match Score 46; DB 4; Length 3461;
 Best Local Similarity 71.4%; Pred. No.: 9c*32;
 Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 3 YPSGNCGLY-YSY 14
 Db 1974 YPGGNIGLYCPYSS 1987

RESULT 8
 US-09-198-452A-7
 Sequence 7, Application US/09198452A
 Patent No. 6559224
 GENERAL INFORMATION:
 APPLICANT: Griffais, R.
 TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
 FILE REFERENCE: 9710-003-999
 CURRENT APPLICATION NUMBER: US/09/198,452A
 CURRENT FILING DATE: 1998-11-24
 NUMBER OF SEQ ID NOS: 6843
 SEQ ID NO 7
 LENGTH: 460
 TYPE: PRT
 ORGANISM: Chlamydia pneumoniae
 US-09-198-452A-7

Query Match Score 43; DB 4; Length 46C;
 Best Local Similarity 60.0%; Pred. No.: 70;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YPSGNCGLY 22
 Db 7 FPGNCGNY 16

RESULT 9
 US-09-328-352-6858
 Sequence 6858, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUmannii FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTG99-C3PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 6058
 LENGTH: 4C9
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-6858

Query Match Score 42; DB 4; Length 4C9;
 Best Local Similarity 100.0%; Pred. No.: 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SGNCGLY 1
 Db 396 SGNCGLY 4C9

RESULT 10
 US-09-933-821-6
 Sequence 6, Application US/08933821
 Patent No. 5972338
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul C.
 TITLE OF INVENTION: Tie Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/C8/933,821
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-3216
 TELEFAX: 650/952-3881
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 470 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 JS-08-933-821-6

Query Match Score 41.5; DB 2; Length 47C;
 Best Local Similarity 60.0%; Pred. No.: 1.2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indels 1;
 Gaps 1;

Qy 1 DRYPSGNCGLYSSG 15
 Db 4C4 JSY-SGNCAQLQRGG 417

RESULT 11
 US-08-960-507-6
 Sequence 6, Application US/08960507
 Patent No. 6057435
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 TITLE OF INVENTION: Tie Ligands
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/96C,507

RESULT 13
 US-09-332-928A-6
 Sequence 6, Application US/09332928A
 Patent No. 6368853
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 Gurney, Austin L.
 TITLE OF INVENTION: Tie Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/332,928A
 FILING DATE: 14-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/933,821
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/952-9881
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 470 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 JS-09-960-507-6

RESULT 12
 US-09-136-828-6
 Sequence 6, Application US/09136828
 Patent No. 635C450
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 Gurney, Austin L.
 TITLE OF INVENTION: Tie Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,828
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130R1A
 TELEPHONE: 650/952-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 470 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 JS-09-136-828-6

Query Match 47.2%; Score 41.5; DB 3; Length: 470;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Query 1 DRYPSGNCGYSSG 15
 Db 404 DSY-SGNCAIYQRGG 417

RESULT 14
 US-09-136-828-6
 Sequence 6, Application US/09136828
 Patent No. 64137C
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 Gurney, Austin L.
 Hillman, Kenneth
 Botstein, David
 Goddard, Audrey
 Roy, Margaret
 Ferrara, Napoleone
 Tumas, Daniel
 APPLICANT: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California

Query Match 47.2%; Score 41.5; DB 4; Length: 470;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Query 1 DRYPSGNCGYSSG 15
 Db 404 DSY-SGNCAIYQRGG 417

COUNTRY: USA
 ZIP: 94180
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DCS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,801
 FILING DATE:
 CLASSIFICATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P130P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-3216
 TELEFAX: 650/952-9882
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 470 amino acids
 TYPE: Amino Acid
 TOPLOGY: Linear

Query Match Score 41.5; DB 4; Length: 470;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 1 DRYPSGNCGIYSSG 15
 Db 404 DSY-SGNCAIYRGG 417

RESULT 15
 US-09-332-929-6
 ; Sequence 6, Application US/09332929

; Patent No. 6420542
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 TITLE OF INVENTION: Tie Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 9418C

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DCS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/332,929
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/933,921
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P130
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 470 amino acids
 TYPE: Amino Acid

TOPLOGY: Linear
 US-09-332-929-6
 Query Match Score 41.5; DB 4; Length: 470;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 1 DRYPSGNCGIYSSG 15
 Db 404 DSY-SGNCAIYRGG 417
 Search completed: November 5, 2003, 16:49:00
 Job time : 2.05727 secs

Result	NC	Score	Query Match Length	DB ID	Description
1	31	35.2	14	2	alpha-conotoxin CG
2	31	35.2	15	1	alpha-conotoxin CG
3	26	29.5	15	2	alpha-conotoxin CG
4	24	27.3	10	2	alpha-conotoxin CG
5	23.5	26.7	12	2	alpha-conotoxin CG
6	6	23	26.1	10	alpha-conotoxin CG
7	7	23	26.1	13	alpha-conotoxin CG
8	23	26.1	14	2	alpha-conotoxin CG
9	23	26.1	15	2	alpha-conotoxin CG
10	23	26.1	15	2	alpha-conotoxin CG
11	23	26.1	15	2	alpha-conotoxin CG
12	22.5	25.6	11	2	alpha-conotoxin CG
13	22	25.6	9	2	alpha-conotoxin CG
14	22	25.0	11	2	alpha-conotoxin CG
15	22	25.0	13	2	alpha-conotoxin CG
16	22	25.0	13	2	alpha-conotoxin CG
17	22	25.0	14	1	alpha-conotoxin CG
18	22	25.0	14	2	alpha-conotoxin CG
19	22	25.0	15	2	alpha-conotoxin CG
20	21	23.9	9	2	alpha-conotoxin CG
21	21	23.9	9	2	alpha-conotoxin CG
22	21	23.9	9	2	alpha-conotoxin CG
23	21	23.9	10	2	alpha-conotoxin CG
24	21	23.9	11	2	alpha-conotoxin CG
25	21	23.9	12	2	alpha-conotoxin CG
26	21	23.9	13	2	alpha-conotoxin CG
27	21	23.9	13	2	alpha-conotoxin CG
28	21	23.9	15	2	alpha-conotoxin CG
29	21	23.9	15	2	alpha-conotoxin CG

Searched: 283309 seqs, 9516852 residues

Total number of hits satisfying chosen parameters: 2520

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Query

Match

Length

DB

ID

Description

RESULT 1

A8963

alpha-conotoxin: CnIA - cone shell: (Corus consors)

N: Contains: alpha-conotoxin CnIB

C: Species: Corus consors

C: Date: 16-Jul-1999 #sequence_revision: 26-Jul-1999 #text_change: 16-Jul-1999

C: Accession: A5863

R: Favreau, F.; Krimm, I.; Le Gail, F.; Boberrieth, M.C.; Lamthanh, H.; Bouet, F.; Serv

B: Biochemistry 38: 6317-6326, 1999

A: Title: Biochemical characterization and nuclear magnetic resonance structure of novel

A: Reference number: A5863; PMID:99255390; PMID:10320362

A: Accession: A5863

A: Status: preliminary

A: Molecule type: Protein

A: Residues: 1-14 <FAV>

C: Superfamily: alpha-conotoxin

C: Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neur

F: 1-14/Product: alpha-Conotoxin CnIB #status: experimental <MTA>

F: 1-14/Product: alpha-Conotoxin CnIB #status: experimental <MTA>

F: 1-14/Modified site: amidated carboxyl end (Cys); #status: experimental

F: 1-14/Modified site: amidated carboxyl end (Cys); #status: experimental

C: Best Local Similarity 63.3%; Pred. No. 1.1e+02; Indels 0; Gaps 0;

Matches 5; Conservative 5; Mismatches 1;

QY 8 CGLYYS 13

Dy 8 CGKYS 13

Db 8 CGKYS 13

C: Best Local Similarity 63.3%; Pred. No. 1.1e+02; Length 14;

Matches 5; Conservative 5; Mismatches 1;

QY 8 CGLYYS 13

Dy 8 CGKYS 13

Db 8 CGKYS 13

C: Best Local Similarity 63.3%; Pred. No. 1.1e+02; Length 14;

Matches 5; Conservative 5; Mismatches 1;

QY 8 CGLYYS 13

Dy 8 CGKYS 13

Db 8 CGKYS 13

C: Best Local Similarity 63.3%; Pred. No. 1.1e+02; Length 14;

Matches 5; Conservative 5; Mismatches 1;

QY 8 CGLYYS 13

Dy 8 CGKYS 13

Db 8 CGKYS 13

C: Best Local Similarity 63.3%; Pred. No. 1.1e+02; Length 14;

Matches 5; Conservative 5; Mismatches 1;

QY 8 CGLYYS 13

Dy 8 CGKYS 13

Db 8 CGKYS 13

C: Best Local Similarity 63.3%; Pred. No. 1.1e+02; Length 14;

Matches 5; Conservative 5; Mismatches 1;

QY 8 CGLYYS 13

Dy 8 CGKYS 13

Db 8 CGKYS 13

GenCore version 5.1.6
Copyright (c) - 1993 - 2003 Computer Ltd.
CM protein - protein search, using sw model
Run on: November 5, 2003, 16:55:36 ; Search: time 20 seconds
without digests;
72.127 Million cell updates/sec
Title: US-09-902-563-18
Perfect score: 88
Sequence: 1 DRYPSNGCGLYSSG 15
Scoring table: BIOSUM62
Gappp 10.0 , Gapext 0.5

ALIGNMENTS

acidic fibroblast
epidermal growth factor
T-cell receptor beta
acetylcholinesterase
IG H chain V-D-J
botulinum neurotoxin
IG heavy chain CRD
IG K chain V-D-J
aspartate transaminase
hypertrehalosemic proteinase chain 1
T-cell receptor alpha
T-cell receptor alpha
porin por 1B - Ara
porin por1 - Ara

submitted to the Brookhaven Protein Data Bank, May 1996

A; Reference number: A66253; PDB:1INC
 A; Contenents: annotation, X-ray crystallography, 1.2 angstroms, residues 1-12
 R; Gudat, L.W.; Martin, C.A.; Shan, S.; Edmundson, A.B.; Gray, W.R.
 Biochemistry 35, 11329-11335, 1996
 A; Title: Three dimers: conformational structure of the alpha-conotoxin GI at 1.2 angstroms resolution
 A; Reference number: A58592; MUID:93138624; PMID:8734187
 A; Contenents: annotation, X-ray crystallography, 1.2 angstroms
 R; Pardi, A.; Gallo, A.; Florance, J.; Manicrete, D.
 Biichemistry 28, 5494-5501, 1989
 A; Title: Solution structures of alpha-conotoxin GI determined by two-dimensional NMR spectroscopy
 C; Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; blocked carboxyl end
 C; Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic
 C; Superfamily: alpha-conotoxin
 C; Keywords: conotoxin GI #status experimental <GIA>
 F;1-13;Product: conotoxin GI #status experimental <GIC>
 F;2-7;3-13;Disulfide bonds: #link GIA #status predicted
 F;2-7;3-13;Disulfide bonds: #link GIC #status experimental
 F;13-/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly)
 F;15/Modified site: blocked carboxyl end (Lys) (probably amidated) #status experimental
 A; Accession: S25024

RESULT 5

S25056
 Query Match Score 24; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1e-03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Cy 8 CGLYSSG 15
 | :| :|
 Db 2 CAVNSSSG 5

Query Match Score 24; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 1e-03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Cy 8 CGLYSSG 15
 | :| :|
 Db 2 CAVNSSSG 5

RESULT 6

PT2413
 Query Match Score 23.5%; DB 2; Length 12;
 Best Local Similarity 46.2%; Pred. No. 1.e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
 Cy 2 RYPGNCGIYSS 14
 | :| :| :|
 Db 2 RYP----YVYGS 9

Query Match Score 23.5%; DB 2; Length 12;
 Best Local Similarity 46.2%; Pred. No. 1.e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
 Cy 2 RYPGNCGIYSS 14
 | :| :| :|
 Db 2 RYP----YVYGS 9

REB6
 PT2413
 Query Match Score 23; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1.e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 7

JTCG3
 tremederogen a13 - jelly fungus (*Tremella mesenterica*)
 C; Species: *Tremella mesenterica*
 C; Date: 03-Aug-1994 #sequence_revision 03-Aug-1994
 C; Accession: A01641
 R; Isikagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.
 Science 212, 1525-1527, 1981
 A; Title: Peptide sex hormones inducing conjugation tube formation in compatible mating
 A; Reference number: A94256

Query Match Score 23; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 1.e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

C41946
 T-cell receptor gamma chain (1t_60) - mouse (fragment)
 C; Species: *Mus musculus* (house mouse);
 C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1993
 C; Accession: C41946
 R; Whetstone, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
 Mol. Cell. Biol. 11, 5902-5909, 1991
 A; Title: Rearrangement and junctional site sequence analyses of T-cell receptor gamma gene
 A; Reference number: A41946; MUID:9249316; PMID:658619
 A; Accession: C41946
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: DNA
 A; Residues: 1-10 <WHE>

Query Match Score 23; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 7.3e-02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Cy 2 DRYPSGRGGL 10
 | :| :| :|
 Db 1 DYERGDGVN 10

Query Match Score 23; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 7.3e-02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Cy 9 GIVYSSG 15
 | :| :|
 Db 2 GIVYSSG 8

us-09-902-563-18.clos d.rpr

1

```

A;Accession: A01641
A;Molecule type: protein
A;Residues: 1-13 <S9K>
C;Comment: Tremorogen a-13 is produced by the a mating-type cells and induces formation
C;Superfamily: tremorogen a-13
C;Keywords: extracellular protein; hormone; lipoprotein; pheromone; prenylated cysteine
F;13;Binding site: farnesyIcys; covalent; #status experimental
F;13;Modified site: methyl ester carboxy-end (Cys); #status absent

Query Match 26.1%; Score 23; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C;Keywords: T-cell receptor

Cy 4 PSGNC 8
      ||| |
Db 9 PGVC 13

RESULT 8
PH0792
T-cell receptor alpha chain (H2 V-alpha-2.7A.9) - mouse (fragment)
C;Species: Mus musculus (house mouse);
C;Accession: PH0792
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R;Casanova, J.L.; Romero, P.; Widmann, C.; Maryanski, C.B.
A;Title: T cell receptor genes in a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoires.
A;Reference number: PH0746; MUID:92078846; PMID:1836610
A;Molecule type: mRNA
A;Cross-references: EMBL:X6CB97
A;Experimental source: T lymphocyte
A;Keywords: T-cell receptor

Query Match 26.1%; Score 23; DB 2; Length 14;
Best Local Similarity 45.5%; Pred. No. 2.1e+03; Length 15;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
C;Keywords: complement alternate pathway; glycoprotein

Cy 5 SGNCGLYSSS 15
      | : | |
        | : | |
Db 4 SANSGTYQRFS 14

RESULT 9
PH1366
IG heavy chain D $\gamma$  region (clone C11-106) - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: PH1366
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
R;Rasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
C;Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type D $\gamma$ H joining in young children with B precursor lymphoma
A;Reference number: PH1302; MUID:93094761; PMID:1463429
A;Accession: PH1366
A;Molecule type: DNA
A;Residues: 1-15 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.2e+03; Length 15;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
C;Keywords: T-cell receptor

Cy 5 SGNCGLYSSS 15
      | : | |
Db 4 SGYYGSDWQGS 14

RESULT 10
PH0750
T-cell receptor beta chain (C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)

Query Match 25.6%; Score 22.5; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 2e+03; Length 11;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
C;Keywords: T-cell receptor

Cy 8 CGY-YSSG 15
      | : | |
Db 2 CAWWRSSG 10

RESULT 11
PH0750
T-cell receptor beta chain (C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)

Query Match 26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.2e+03; Length 15;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
C;Keywords: T lymphocyte

Cy 4 PGNCGLY 12
      | : | |
Db 5 PGNTGOLY 13

RESULT 12
PH1110
complement factor B1-Bb and B2-Bb - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Accession: PH1110
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 15-Nov-1996
R;Matsushita, M.; Okada, H.
A;Title: Two forms of guinea pig factor S of the alternative complement pathway with different immunological properties.
A;Reference number: A93136; MUID:8384686; PMID:2779589
A;Accession: PL0110
A;Molecule type: protein
A;Residues: 1-15 <NAT>
C;Keywords: complement alternate pathway; glycoprotein

Query Match 26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 2.2e+03; Length 15;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
C;Keywords: complement alternate pathway; glycoprotein

Cy 4 PGNCGLY 11
      | : | |
Db 6 PGSKNY 13

RESULT 13
PH0750
R;Whetell, M.; Mosley, R.L.; Whetell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: B41946
A;Molecule type: DNA
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-11 <WES>
C;Keywords: T-cell receptor

Query Match 25.6%; Score 22.5; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 2e+03; Length 11;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
C;Keywords: T-cell receptor

Cy 8 CGY-YSSG 15
      | : | |
Db 2 CAWWRSSG 10

```

S19323 spermactivating peptide SAP - sea urchin (Stomopneustes variolus);
 C;Species: Stomopneustes variolus
 C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Aug-2000
 C;Accession: S19329
 R;Yoshino, K.; Takao, T.; Shimonishi, Y.; Suzuki, N.
 A;Title: Determination of the amino acid sequence of an intramolecular disulfide linkage
 A;Reference number: S19329; PMID:1756856
 A;Accession: S19329
 A;Molecule type: protein
 A;Residues: 1-5 <YGS>
 C;Superfamily: unassigned animal peptides
 F;3-8/Disulfide bonds: #status predicted

Query Match Score 25.0%; Best Local Similarity 50.0%; Pred. No. 2.8e+03; Score 22; DB 1; Length 13;
 Best Local Similarity Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 8 CSBYYS 13
 Db 7 CGKHF 12

Search completed: November 5, 2003, 16:59:09
 Job time : 22 secs

RESULT 14
 PTO302 Ig heavy chain CRD3 region (clone 5.1.2) - human (fragment)
 C;Species: Homo sapiens (man);
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1995
 C;Accession: PTO302
 R;Yamada, Y.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173: 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A;Reference number: PT0222; PMID:9108337; PMID:183302
 A;Accession: PTO302
 A;Molecule type: DNA
 A;Residues: 1-->YAM,
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer, immunoglobulin

Query Match Score 25.0%; Best Local Similarity 71.4%; Pred. No. 2.4e+03; Score 22; DB 2; Length 11;
 Best Local Similarity Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 9 GAYSSG 15
 Db 3 GPRSSSG 9

RESULT 15
 NTXN2G alpha-conotoxin GI - cone shell ('Conus geographus')
 C;Species: Conus geographus (geographic cone)
 C;Date: 24-Sep-1991 #sequence_revision 24-Sep-1991 #text_change 23-May-1997
 C;Accession: A01783
 R;Gray, W.R.; Luque, A.; Olivera, S.M.; Barrett, J.; Cruz, L.J.
 J. Biol. Chem. 256: 4744-4740, 1981
 A;Title: Peptide toxins from Conus geographus venom
 A;Reference number: A92120; PMID:8191854; PMID:704556
 A;Accession: A01783
 A;Molecule type: protein
 A;Residues: 1-13 <GRA>
 R;Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, F.M.
 J. Biol. Chem. 258: 12241-12251, 1983
 A;Title: Conotoxin MI: Disulfide bonding and conformational states.
 A;Reference number: A92196; PMID:8434400; PMID:6636187
 A;Comments: annotation: disulfide bonds
 C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic
 C;Superfamily: alpha-conotoxin
 C;Keywords: acetylcholine receptor inhibitor; blocked carboxyl end; postsynaptic neurotransmitter
 F;2,7,3-13/Disulfide bonds: #status predicted
 F;13/Modified site: blocked carboxyl end (cys) (probably amidated) #status experimental

Result No.	Score	Query	Match Length	DB ID	Description
1	31	CXAI_CCNCON	14	1	P56973 corus conso
2	31	CXAI_CCNCON	15	1	P01519 corus georg
3	26	CXAI_CCNCON	15	1	P19897 bacteriorpha
4	23	CXAI_CCNCON	13	1	P01370 tremella me
5	23	CXAI_CCNCON	14	1	P29399 alermonnas
6	23	CXAI_CCNCON	15	1	P0C620 zeia mays
7	22	CXAI_CCNCON	9	1	S24C47 stomopneute
8	22	CXAI_CCNCON	13	1	P01520 corus georg
9	22	CXAI_CCNCON	14	1	FC1521 corus magus
10	21	CXAI_CCNCON	9	1	P81726 leucophaea
11	21	CXAI_CCNCON	15	1	P31720 rattus norv
12	21	CXAI_CCNCON	15	1	P18651 caris famili
13	20	CXAI_CCNCON	10	1	P05025 fasciola he
14	19	CXAI_CCNCON	9	1	P16223 fasciola he
15	19	CXAI_CCNCON	10	1	P16353 heliothis z
16	19	CXAI_CCNCON	14	1	P45661 leurus qui
17	19	CXAI_CCNCON	15	1	P34072 tremella br
18	19	CXAI_CCNCON	15	1	P280612 zeia mays
19	18	CXAI_CCNCON	10	1	P81731 helicoverpa
20	18	CXAI_CCNCON	13	1	P40928 homo sapien
21	18	CXAI_CCNCON	14	1	P80342 fasciola he
22	18	CXAI_CCNCON	20.5	1	P01555 sus scrofa
23	16	CXAI_CCNCON	14	1	Q04303 bacillus i
24	16	CXAI_CCNCON	15	1	P21918 lumbricus
25	18	CXAI_CCNCON	20.5	1	P80625 zeia mays
26	17	CXAI_CCNCON	19.3	8	P82152 clydonia pomon
27	17	CXAI_CCNCON	9	1	P19930 leucophaea
28	17	CXAI_CCNCON	19.3	8	P242999 sclerites aca
29	17	CXAI_CCNCON	19.3	9	P28278 oryctocephalus
30	17	CXAI_CCNCON	19.3	10	P28278 macrobrachium
31	17	CXAI_CCNCON	19.3	12	P56809 corus marmo
32	17	CXAI_CCNCON	19.3	14	P80732 streptocyte
33	17	CXAI_CCNCON	19.3	15	P81285 matrestra br

ALIGNMENTS					
Scoring table:	BLOSUM62	Gapop 10.0	Gapexi 3.5		
Searched:	127863 seqs.	47026715 residues			
Total number of hits satisfying Chosen parameters:	725				
Minimum DB seq length:	0				
Maximum DB seq length:	15				
Post-processing:	Minimum Match: 0%				
	Maximum Match: 100%				
	Listing First 45 summaries				
Database :	SwissProt_41:				
Result No.	Score	Query	Match Length	DB ID	Description
1	35.2	CXAI_CCNCON	14	1	P56973 corus conso
2	31	CXAI_CCNCON	15	1	P01519 corus georg
3	26	CXAI_CCNCON	15	1	P19897 bacteriorpha
4	23	CXAI_CCNCON	13	1	P01370 tremella me
5	23	CXAI_CCNCON	14	1	P29399 alermonnas
6	23	CXAI_CCNCON	15	1	P0C620 zeia mays
7	22	CXAI_CCNCON	9	1	S24C47 stomopneute
8	22	CXAI_CCNCON	13	1	P01520 corus georg
9	22	CXAI_CCNCON	14	1	FC1521 corus magus
10	21	CXAI_CCNCON	9	1	P81726 leucophaea
11	21	CXAI_CCNCON	15	1	P31720 rattus norv
12	21	CXAI_CCNCON	23.9	15	P18651 caris famili
13	20	CXAI_CCNCON	22.7	10	P05025 fasciola he
14	19	CXAI_CCNCON	21.6	9	P16223 fasciola he
15	19	CXAI_CCNCON	21.6	10	P16353 heliothis z
16	19	CXAI_CCNCON	21.6	14	P45661 leurus qui
17	19	CXAI_CCNCON	21.6	15	P34072 tremella br
18	19	CXAI_CCNCON	21.6	15	P280612 zeia mays
19	18	CXAI_CCNCON	20.5	10	P81731 helicoverpa
20	18	CXAI_CCNCON	20.5	13	P40928 homo sapien
21	18	CXAI_CCNCON	20.5	14	P80342 fasciola he
22	18	CXAI_CCNCON	20.5	14	P01555 sus scrofa
23	16	CXAI_CCNCON	20.5	14	Q04303 bacillus i
24	16	CXAI_CCNCON	15	1	P21918 lumbricus
25	18	CXAI_CCNCON	20.5	15	P80625 zeia mays
26	17	CXAI_CCNCON	19.3	8	P82152 clydonia pomon
27	17	CXAI_CCNCON	9	1	P19930 leucophaea
28	17	CXAI_CCNCON	19.3	8	P242999 sclerites aca
29	17	CXAI_CCNCON	19.3	9	P28278 oryctocephalus
30	17	CXAI_CCNCON	19.3	10	P28278 macrobrachium
31	17	CXAI_CCNCON	19.3	12	P56809 corus marmo
32	17	CXAI_CCNCON	19.3	14	P80732 streptocyte
33	17	CXAI_CCNCON	19.3	15	P81285 matrestra br

SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.					
Scoring table:	BLOSUM62	Gapop 10.0	Gapexi 3.5		
Searched:	127863 seqs.	47026715 residues			
Total number of hits satisfying Chosen parameters:	725				
Minimum DB seq length:	0				
Maximum DB seq length:	15				
Post-processing:	Minimum Match: 0%				
	Maximum Match: 100%				
	Listing First 45 summaries				
Database :	SwissProt_41:				
Result No.	Score	Query	Match Length	DB ID	Description
1	35.2	CXAI_CCNCON	14	1	P56973 corus conso
2	31	CXAI_CCNCON	15	1	P01519 corus georg
3	26	CXAI_CCNCON	15	1	P19897 bacteriorpha
4	23	CXAI_CCNCON	13	1	P01370 tremella me
5	23	CXAI_CCNCON	14	1	P29399 alermonnas
6	23	CXAI_CCNCON	15	1	P0C620 zeia mays
7	22	CXAI_CCNCON	9	1	S24C47 stomopneute
8	22	CXAI_CCNCON	13	1	P01520 corus georg
9	22	CXAI_CCNCON	14	1	FC1521 corus magus
10	21	CXAI_CCNCON	9	1	P81726 leucophaea
11	21	CXAI_CCNCON	15	1	P31720 rattus norv
12	21	CXAI_CCNCON	23.9	15	P18651 caris famili
13	20	CXAI_CCNCON	22.7	10	P05025 fasciola he
14	19	CXAI_CCNCON	21.6	9	P16223 fasciola he
15	19	CXAI_CCNCON	21.6	10	P16353 heliothis z
16	19	CXAI_CCNCON	21.6	14	P45661 leurus qui
17	19	CXAI_CCNCON	21.6	15	P34072 tremella br
18	19	CXAI_CCNCON	21.6	15	P280612 zeia mays
19	18	CXAI_CCNCON	20.5	10	P81731 helicoverpa
20	18	CXAI_CCNCON	20.5	13	P40928 homo sapien
21	18	CXAI_CCNCON	20.5	14	P80342 fasciola he
22	18	CXAI_CCNCON	20.5	14	P01555 sus scrofa
23	16	CXAI_CCNCON	20.5	14	Q04303 bacillus i
24	16	CXAI_CCNCON	15	1	P21918 lumbricus
25	18	CXAI_CCNCON	20.5	15	P80625 zeia mays
26	17	CXAI_CCNCON	19.3	8	P82152 clydonia pomon
27	17	CXAI_CCNCON	9	1	P19930 leucophaea
28	17	CXAI_CCNCON	19.3	8	P242999 sclerites aca
29	17	CXAI_CCNCON	19.3	9	P28278 oryctocephalus
30	17	CXAI_CCNCON	19.3	10	P28278 macrobrachium
31	17	CXAI_CCNCON	19.3	12	P56809 corus marmo
32	17	CXAI_CCNCON	19.3	14	P80732 streptocyte
33	17	CXAI_CCNCON	19.3	15	P81285 matrestra br

RESULT 2
CXAI_CONGE

ID AC	CXAI CONGE STANDARD;	PR ^r ;	15 AA.	
DT 21-JUL-1986 (Rei. 01; Created)				
DT 21-JUL-1986 (Rei. 01; Last sequence update)				
DT 15-SEP-2003 (Rei. 42; Last annotation update)				
DE Alpha-conotoxin GI [Contains: Alpha-conotoxin GI (31)].				
CS Conus geographus (Geography cone).				
OC Lukuyota Metaoa; Mollusca; Gastropoda; Orthogastropoda;				
CC Neogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;				
CC Conidae; Conoidea; Conidae; Comidae;				
OX NCBI Taxid: 6491;				
RN				
RP SEQUENCE.				
RX MEDLINE=81:191854; PubMed=7014556;				
RA Gray W.R., Luque F.A., Olivera B.M., Barreto J., Cruz L.J., Cruz L.J., "Peptide toxins from Conus geographus venom.", J. Biol. Chem. 256:4734-4740(1981).				
RX DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.				
RX MEDLINE=93:10594; PubMed=7152021;				
RA Nishizuchi Y., Sakakibara S., "Primary and secondary structure of conotoxin GI, a neurotoxic tridecapeptide from a marine snail.", Peptides Lett. 12: 248-260(1982).				
RN				
RP DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.				
RX MEDLINE=84:280842; PubMed=646616;				
RA Gray W.R., Luque F.A., Gaiyam R., Atherton E., Sheppard R.C., Cruz L.J., Reyes A., Alford J., McIntosh M., Olivera B.Y., Cruz L.J., "Conotoxin GI: disulfide bridges, synthesis, and preparation of iodinated derivatives.", Biochemistry 23:2795-2802(1984).				
RN	[4]			
RP COMPARISON WITH ALPHA-CONOTOXIN SI AND ALPHA-CONOTOXIN MI.				
RX MEDLINE=93:034819; PubMed=7947815;				
RA Hann R.M., Pagan J.R., Eterovic V.A.; Grobe D.R., Dunn J.M., Levitan E.S., Abramson S.N.; RT "alpha-Conotoxins GI and MI distinguish one of the two nicotinic acetylcholine receptor agonist sites while SI does not.", Biochemistry 33:14058-14063(1994).				
RN	[5]			
RP PHARMACOLOGICAL CHARACTERIZATION ON MOUSE MUSCLE-DERIVED BC3H-1 CELLS AND TORPEDO ELECTRIC ORGAN.				
RX MEDLINE=93:149316; PubMed=6227764;				
RA Gudde L.W., Dunn J.M., Levitan E.S., Abramson S.N.; RT "Determinants involved in the affinity of alpha-conotoxins GI and SI for the muscle subtypes of nicotinic acetylcholine receptors.", Mol. Pharmacol. 48:105-111(1995).				
RN	[6]			
RP MUTAGENESIS OF ARG-9.				
RX MEDLINE=93:17090; PubMed=9174364;				
RA Grobe D.R., Gray W.R., Abramson S.N.; RT "Three-dimensional structure of the alpha-conotoxin GI at 1.2 Å resolution.", Biochemistry 35:ii1329-ii1335(1996).				
RN	[8]			
RP X-RAY CRYSTALLOGRAPHY (1.2 ANGSTROMS) CP GI.				
RX MEDLINE=93:7864; PubMed=276554;				
RA Kobayashi Y., Ohkubo T., Kyogoku Y., Nishizuchi Y., Sakakibara S., Braun W., Go N.; RT "Solution conformation of conotoxin GI determined by 1H nuclear magnetic resonance spectroscopy and distance geometry calculations.", Biochemistry 28:4851-4860(1989).				
RN	[9]			
RP STRUCTURE BY NMR OF GI.				
RX MEDLINE=83:352562; PubMed=276554;				
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RP STRUCTURE BY NMR OF GI.				
RX MEDLINE=83:352562; PubMed=276554;				
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RX MEDLINE=83:352562; PubMed=276554;				
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RP STRUCTURE BY NMR OF GI.				
RX MEDLINE=83:352562; PubMed=276554;				
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PROTEIN IS: 5.9, ITS MW IS: 34.6 kDa.

DR Maize-2DPAGE; P08620; COLEOPTILE.

DR MaizedB; 123944; -.

FT NON-TER 1

FT NON-TER 15

FT NON-TER 15 AA; 1564 MW; CFCGBAAJBD5658 CRC64;

FT SEQUENCE 15 AA;

Query Match. Best Loca: Similarity 26.1%; Score 23; DB 1; Length 15; Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GNGCLYY 12

Ds 4 GDGGAYY 1C

RESULT 7

ID_SAP_STOVA STANDARD; PRT; 9 AA.

AC P246047;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 01-MAR-1992 (Rel. 21, Last annotation update)

DE Spasm-activating Peptide (SAP).

OS Stomopneutes variolarius (Sea urchin).

OC Eukaryota; Metazoa; Echinodermata; Eublatherzoa; Echinozoa; Stomopneutes; Euechinoidea; Diadematacea; Phymosomatoida; Stenomechinidae;

OC Echinoidida; Euechinoidea; Diadematacea; Phymosomatoida; Stenomechinidae;

OX NCBI_TaxID=1663;

RN [1]

RP SEQUENCE, AND DISULFIDE BOND.

RX MEDLINE=92097763; PubMed=17565658;

RA Yoshimoto K.-I., Takao T., Shimomoto Y., Suzuki N.;

RT "Determination of the amino acid sequence of an intramolecular disulfide linkage-containing sperm-activating peptide by tandem mass spectrometry";

RL FEBS Lett. 294:179-182 (1991).

CC !- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF cAMP, cGMP AND CLASICU LEVELS IN SPERM CELLS, AND TRANSIENT ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF GUANYLATE CYCLASE.

FT DISULFID 3 8

SC SEQUENCE 9 AA; 1010 MW; C469B3387B0765B9 CRC64;

Query Match. Best Local Similarity 25.0%; Score 22; DB 1; Length 9; Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PSGNCS 8

Ds 4 PEGKCS 8

RESULT 8

ID_CXA2 CONGE STANDARD; PRT; 13 AA.

AC P01520;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-conotoxin GI.

OS Conus geographus (Geography cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeocochlea; Hypsogastropoda;

OC Negastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=6491;

RN [1]

RP SEQUENCE, MEDLINE=9119-054; PubMed=7014556;

RX Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;

RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;

RT "Peptide toxins from Conus geographus venom.";

RP J. Biol. Chem. 256:4734-4740 (1981).

RN [2]

RP DISULFIDE BONDS.

RX MEDLINE=84280842; PubMed=6666616;

RA Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C., Cruz L.J., Reyes A., Alford J., McIntosh M., Olivera B.M., Stone B.L., Rivier J.

RA "Conotoxin GI: disulfide bridges, synthesis, and preparation of iodinated derivatives.";

RT Biochemistry 23:296-2802 (1984).

CC !- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.

CC !- TISSUE SPECIFICITY: Expressed by the venom duct.

CC !- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE FAMILY.

CC PIR; A01783; NTKN2G.

DR HSSP; P65973; 1B45.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;

KW Acetylcholine receptor inhibitor; Amidation.

FT DISULFID 2 7

FT DISULFID 3 13

FT MOD_RES 13 13 AMIDATION.

SO SEQUENCE 13 AA; 1422 MW; DEEBE831C39297EBD CRC64;

Query Match. Best Local Similarity 25.0%; Score 22; DB 1; Length 13; Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CGLYYS 13

Ds 7 CGKFRS 12

RESULT 9

ID_CXA1_CCNA STANDARD; PRT; 14 AA.

AC P01521;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-conotoxin MI (MI).

OS Conus magus (Magus cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeocochlea; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=6492;

RN SEQUENCE,

RP MEDLINE=93073458; PubMed=7149738;

RA McIntosh J.M., Cruz L.J., HurkaPiller M.W., Gray W.R., Olivera B.M.;

RT "Isolation and structure of a peptide toxin from the marine snail Conus matus.";

RC Arch. Biochem. Biophys. 218:329-334 (1982).

RN DISULFIDE BCNDS.

RX MEDLINE=94032400; PubMed=6661C187;

RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;

RT "Conotoxin MI: Disulfide bonding and conformational states.";

RL J. Biol. Chem. 258:12247-12251 (1983).

CC !- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.

CC !- SUBCELLULAR LOCATION: Secreted.

CC !- TISSUE SPECIFICITY: Expressed by the venom duct.

CC !- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE FAMILY.

CC PIR; A01784; NTKN1M.

DR HSSP; P65973; 1B45.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;

KW Acetylcholine receptor inhibitor; Amidation.

FT DISULFID 3 8

FT DISULFID 4 14 AMDATION
 SQ MOD RES 14 AA; 14 AA; DEDE91898BF555BD CRC64;

Query Match Score 22; DB 1; Length 14;
 Best Local Similarity 66.7%; Prod. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 8 CGLYYS 13
 Db 8 CGGNYS 13

RESULT 10
 TRP4-LEIMA STANDARD; PRT; 9 AA.
 ID TRP4 LEIMA
 AC PB-736;
 DT 30-MAY-2000 (Rel. 39; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 15-SEP-2003 (Rel. 42; Last annotation update)
 DE "Tachykinin-related peptide 4 (LeuMRF-4)."
 OS Leucophiinae maderae (Madeira cockroach).
 OC Neoptera: Orthopteroidea: Dictyoptera: Blattaria: Blaberoidea;
 OC Blaberidae; Leucophiinae.
 OX NCBI_TaxID=6988;
 RN [1]

RP SEQUENCE
 RC TISSUE_Midgut;
 RX MEDLINE=97233012; PubMed=8897641;

RA Muren J.E., Naesel D.P.;
 RT "Isolation of five tachykinin-related peptides from the midgut of cockroach Leucophiinae maderae: existence of N-terminally extended isoforms.";
 RL Regul. Pept. 65:185-196 (1996).

CC FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.

CC "SIMILARITY: SECRETED."
 CC "Tissue Specificity: Midgut."
 CC "SIMILARITY: SOME SIMILARITY TO TACHYKININS."
 KW Tachykinin; Neuropeptide; Amidation.

FT MOD_RES 9 9 AMDATION
 SQ SEQUENCE 9 AA; 953 MW; 240387699C8E65A7 CRC64;

Query Match Score 23.9%; DB 1; Length 9;
 Best Local Similarity 57.1%; Prod. No. 1.3e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 4 PSQNGL 1C
 Ds 2 PSQFMGM 8

RESULT 11
 C1QA_RAT STANDARD; PRT; 15 AA.
 ID C1QA_RAT
 AC P31723;
 DT 01-JUL-1993 (Rel. 26; Created)
 DT 01-JUL-1993 (Rel. 26; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Complement C1q subcomponent, A chain (Fragment).

GN Rattus norvegicus (Rat);
 OC Bickartova; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 OX NCBI_TaxID=10116;
 RN [1]

RF MEDLINE=93218657; PubMed=9464426;
 RA Wang M.G., Seilley D.J., Bridgman D.J., Harrision E.A.;
 RT "Rapid isolation and biochemical characterization of rat C1 and C1q.";
 RL No. Immunol. 30:433-440 (1993).

CC "SIMILARITY: C1Q ASSOCIATES WITH THE PROENZYME C1R AND C1S TO YIELD

CC C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE C4(2+)-DEPENDENT C1R(2)C1S(2) PHORENYL COMPLEX, AND THE EFFICIENT ACTIVATION OF C1-TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IgG OR IgM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
 CC -!!- SUBJECT: C1 IS A CALCIUM DEPENDENT TRIMOLECULAR COMPLEX OF C1q, R AND S IN THE MOLEAR RATIO OF 1:2:2. THE C1q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN. IN ADDITION TO THE MAJOR A:B AND C:C DIMER BANDS, RAT, UNLIKE HUMAN C1Q, CONTAINED MINOR DIMER SPECIES.
 CC -!!- SIMILARITY: Contains 1 collagenous domain.
 DR InterPro: IPR001073; C1Q.
 DR PROSITE: PS01113; C1Q; PARTIAL.
 DR KIAA Complete; pathway: Plasma; Hydroxylation; Glycoprotein; Collagen;
 DR Repeat.
 DR DISULFID 4 4 INTERCHAIN (WITH C-4 IN B CHAIN).
 FT NCN_TER 15 15
 FT SEQUENCE 15 AA; 1488 MW; 1B3D90008793965 CRC64;
 DR Query Match: 23.9%; Score 21; DB 1; Length 15;
 DR Best Local Similarity 44.4%; Prod. No. 1.5e+03;
 DR Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 CY 2 RYPSRNQGL 10
 DR 3 RAPNSKDGV 13

RESULT 12
 FGFI_CANFA STANDARD; PRT; 15 AA.
 AC P18651;
 DT 01-NOV-1990 (Rel. 16; Created)
 DT 01-NOV-1990 (Rel. 16; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Hepatin-binding growth factor 1 (HBGF-1) (Acidic fibroblast growth factor) (AFGF) (Alpha-endothelial cell growth factor) (Fragment).
 DE GN FGFI OR FGF-2;
 CS Canis familiaris (Dog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 CX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=9231704; PubMed=2714282;
 RA Quinkler W., Maasberg M., Bernotat-Darieciowski S., Luethe N., Sharma H.S., Schaper W.;
 RT "Isolation of heparin-binding growth factors from bovine, porcine and canine hearts";
 RL Eur. J. Biochem. 181:61-73 (1989);
 CC -!!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -!!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY THAN DOES BFGF.
 CC -!!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 DR PIR: S01955; S03955;
 DR InterPro: IPR02343B; IIL_HBGF.
 DR PROSITE; PS00247; HBGF_FGF; PARTIAL.
 DR KIAA Sequence: 15 AA; 1732 MW; 53CC9A3CADDAAA1 CRC64;
 DR Best Local Similarity 66.7%; Prod. No. 1.e+03;
 DR Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CY 1C LYSSG 15
 DR 3 LYXNG 13

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file:          US-69-902-563-16
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searched:      352
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maximum DB seq length: 15

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Listing First 45 summaries


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1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_micr:*
8: sp_organism:*
9: sp_shape:*
10: sp_plant:*
11: sp_rabbit:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriac:*
```

... sp-anear. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

גלאם

SUMMARIES						
Result	No.	Score	Query Match Length	DB	ID	Description
1	27	30.7	10	10	P82419	P82419 ricot
2	25	28.4	13	5	Q8T6E9	Q8t6e9 dirosop
3	25	28.4	13	5	QAST-5	Qast-5 circlop
4	24	27.3	9	4	Q967-78	Q967-78 horo s
5	24	27.3	11	2	Q9AIY6	Q9aiy6 carson
6	24	27.3	11	5	Q9NL65	Q9nl65 ascaris
7	23	26.1	14	13	Q8JJ780	Q8-80 sterep
8	22	25.0	10	6	Q6WP04	Q6wp04 ateles
9	22	25.0	11	13	Q9CWA2	Q9cw02 gallus
10	22	25.0	15	4	Q00604	Q00604 home s
11	22	25.0	15	8	Q95770	Q95770 cyclurus
12	22	25.0	13	13	Q9PR29	Q9pr29 microt
13	21	23.9	10	13	Q9OY93	Q9oy93 gallus
14	21	23.9	13	4	Q9UPE7	Q9upe7 home s
15	21	23.9	13	10	Q8CJ33	Q8cj33 mus m
16	21	23.9	15	10	Q8SV7	Q8sv7 avir

Q8ney9	homo sapien
Q93u4	escherichia
Q9un9	homo sapien
Q9wz6	mus musculu
P82608	rattus norv
Q45876	clostridium
Q45872	clostridium
Q9y99	murine hepa
Q9y51	homo sapien
Q86849	lymphocytic
Q86665	lymphocytic
Q86667	lymphocytic
Q9cb3	arabidopsis
Q9tc3	oryctolagus
Q15342	homo sapien
Q9uc27	homo sapien
Q9uc27	thermococcus
Q9sb4	zea mays (m
Q9tr7	bos taurus
Q9qpt0	mus musculu
Q8879	mus musculu
Q9x33	escherichia
Q9x54	leucania
Q48459	klebsiella
Q9tm2	aplysia cal
Q86656	lymphocytic
Q86664	lymphocytic
Q86668	lymphocytic

ALIENENTS

RESULT 1	PB2436	PB2436	PRELIMINARY;	PRT;	10 PA.
	AC	PB2436;			
	DT	01-JUN-2000	(TREMBLrel. 14, Created)		
	DT	01-JUN-2000	(TREMBLrel. 14, Last sequence update)		
	DT	01-JUN-2000	(TREMBLrel. 14, Last annotation update)		
	DB	50 kDa cell wall protein (Fragment).			
	QS	Nicotiana tabacum (Common tobacco)			
	CC	Eukarya; Viridiplantae; Streptophyta; Embryophyta; eudicots; core eudicots;			
	CC	Spermatophyta; Magnoliophyta; eudicotsyledons; Solanales; Nicotianaceae; Nicotiana.			
	CC	Asteridae; lamiids; Soianales; Solanaceae; Nicotiana.			

{1}	RN	SEQUENCE.
	RP	PETIT BRAVANA;
	RC	RA, Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
	RA	Wojtaszek P., Bolwell G.P.;
	PA	"Proteomic study of secondary cell wall proteins from transformed
	RT	tobacco culture";
	RT	Planta C-10 (2000).
	CC	-- SUBCELLULAR LOCATION: CELL WALL.
	CC	-- TISSUE SPECIFICITY: XYLEM.
	CW	Cell wall.
	KW	NON-TER.
	FT	10
	SQ	SEQUENCE 1C AA; 1126 MW;
		C68B32488AF77B46 CRC64;

AC Q8T6E9; DR 01-JUN-2002 (TREBLE1); 2.; Created;
 ET 01-JUN-2002 (TREBLE1); 2.; Last sequence update;
 DT 01-OCT-2002 (TREBLE1); 22.; Last annotation update;
 DE "Evolutionary genomics of inversions in *Drosophila* pseudoobscura : Nodes of selection".
 GN MYEF2.
 CS *Drosophila miranda* (Fruit fly); Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Eukaryota; Metazoa; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydcoidea; Drosophilidae; *Drosophila*.
 OX NCBI_TAXID=7229;
 RN 11
 RP SEQUENCE FROM N_A.
 RA Schaeffer S.W., Goetting-Minesky M.P., Kovacevic M., Peoples J.,
 RA Graybill J.L., Miller C.M., Kim K., Nelson J.G., Anderson K.W.;
 RT "Evolutionary genomics of inversions in *Drosophila* pseudoobscura : Nodes of selection".
 RT Submitted (JAN-2002); to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF47681:7; AAL91763:1;
 DR FlyBase; FBgn02329; Cmrl\Yef2.
 FT NON-TER 13 13 ;
 FT NON-TER 13 13 MW; 15BF380B6BE05050 CRC64;
 SQ SEQUENCE 13 AA; 13:3 MW; 15BF380B6BE05050 CRC64;
 3;

Query Match Similarity 23.4%; Score 25; DB 5; Length 13;
 Best Local Similarity 8C.0%; Pred. No. 1.7e+C3;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 YPGSN 7
 Db 8 YPGS 12

RESULT 3

Q8STIS_ PRELIMINARY; PRT; 13 AA.
 AC Q8STIS_;
 AC Q8STIS_;
 DT 01-JUN-2002 (TREBLE1); 2.; Created;
 DT 01-JUN-2002 (TREBLE1); 21.; Last sequence update;
 DT 01-OCT-2002 (TREBLE1); 22.; Last annotation update;
 DE "Evolutionary enhancing factor 2 (Fragment).
 GN MYEF2.
 CS *Drosophila pseudobscura* (Fruit fly);
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydcoidea; Drosophilidae; *Drosophila*.
 RN 11
 RP SEQUENCE FROM N_A.
 RA Schaeffer S.W., Goetting-Minesky M.P., Kovacevic M., Peoples J.,
 RA Graybill J.L., Miller C.M., Kim K., Nelson J.G., Anderson K.W.;
 RT "Evolutionary genomics of inversions in *Drosophila* pseudoobscura : Nodes of selection".
 RT Submitted (JAN-2002); to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF476728; AAL91726:1;
 DR EMBL; AF476729; AAL91727:1; -;
 DR EMBL; AF476730; AAL91728:1; -;
 DR EMBL; AF476731; AAL91729:1; -;
 DR EMBL; AF476732; AAL91730:1; -;
 DR EMBL; AF476733; AAL91731:1; -;
 DR EMBL; AF476734; AAL91732:1; -;
 DR EMBL; AF476735; AAL91733:1; -;
 DR EMBL; AF476736; AAL91734:1; -;
 DR EMBL; AF476737; AAL91735:1; -;
 DR EMBL; AF476738; AAL91736:1; -;
 DR EMBL; AF476739; AAL91737:1; -;
 DR EMBL; AF476740; AAL91738:1; -;
 DR EMBL; AF476741; AAL91739:1; -;
 DR EMBL; AF476742; AAL91740:1; -;
 DR EMBL; AF476743; AAL91741:1; -;
 DR EMBL; AF476744; AAL91742:1; -;
 DR EMBL; AF476745; AAL91743:1; -;
 DR EMBL; AF476746; AAL91744:1; -;

EMBL; AF476747; AAL91745:1;
 EMBL; AF476748; AAL91746:1;
 DR EMBL; AF476749; AAL91747:1;
 EMBL; AF476750; AAL91748:1;
 DR EMBL; AF476751; AAL91749:1;
 EMBL; AF476752; AAL91750:1;
 EMBL; AF476753; AAL91751:1;
 EMBL; AF476754; AAL91752:1;
 EMBL; AF476755; AAL91753:1;
 EMBL; AF476756; AAL91754:1;
 EMBL; AF476757; AAL91755:1;
 EMBL; AF476758; AAL91756:1;
 EMBL; AF476759; AAL91757:1;
 EMBL; AF476760; AAL91758:1;
 EMBL; AF476761; AAL91759:1;
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 EMBL; AF476765; AAL91763:1;
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 EMBL; AF476776; AAL91777:1;
 EMBL; AF476777; AAL91778:1;
 EMBL; AF476778; AAL91779:1;
 EMBL; AF476779; AAL91777:1;
 EMBL; AF476780; AAL91778:1;
 EMBL; AF476781; AAL91779:1;
 EMBL; AF476782; AAL91780:1;
 EMBL; AF476783; AAL91781:1;
 EMBL; AF476784; AAL91782:1;
 EMBL; AF476785; AAL91783:1;
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 EMBL; AF476790; AAL91788:1;
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 EMBL; AF476793; AAL91791:1;
 EMBL; AF476794; AAL91792:1;
 EMBL; AF476795; AAL91793:1;
 EMBL; AF476796; AAL91794:1;
 EMBL; AF476797; AAL91795:1;
 EMBL; AF476798; AAL91796:1;
 EMBL; AF476799; AAL91797:1;
 EMBL; AF476800; AAL91798:1;
 EMBL; AF476801; AAL91799:1;
 EMBL; AF476802; AAL91800:1;
 EMBL; AF476803; AAL91801:1;
 EMBL; AF476804; AAL91802:1;
 EMBL; AF476805; AAL91803:1;
 EMBL; AF476806; AAL91804:1;
 EMBL; AF476807; AAL91805:1;
 EMBL; AF476808; AAL91806:1;
 EMBL; AF476809; AAL91807:1;
 EMBL; AF476810; AAL91808:1;
 EMBL; AF476811; AAL91809:1;
 EMBL; AF476812; AAL91810:1;
 EMBL; AF476813; AAL91811:1;
 EMBL; AF476814; AAL91812:1;
 EMBL; AF476815; AAL91813:1;
 EMBL; AF476816; AAL91814:1;
 EMBL; FBgn062298; OpenMet2.
 FN NON_TER 1 1
 FT NON_TER 13 13

Qy	9 GLYYS 14 : : 2 GMYFST 7	RESULT 8 CawP04 PRELIMINARY; PRT; 10 AA. ID Q8WPC4; PRELIMINARY; PRT; 10 AA. AC 01-MAR-2002 ("TREMBrel": 20, Created) DT 01-MAR-2002 ("TREMBrel": 20, Last sequence update) DT 01-MAR-2002 ("TREMBrel": 20, Last annotation update) DE Oculocutaneous albinism type II (Fragment). GN Atelopus belzebul charek (Chamek spider monkey). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TaxID:118643; RN 11; RP SEQUENCE FROM N.A.; PubMed=11778686; RX EMBL:AF336947; PA Seuarez H.N.; Lima C.R.; Lemos B.; Borvicio C.R.; Moreira M.A.Y., CA Navarez F.C.; RT "Gene assignment in Atelopus pariscus chamek (Platyrrhini, Primates); RT Allocation of 18 markers of human syntenic groups 1,2,7,14,15,17 and RT 22."; RL Chromosome Res. 9:631-639(2001). DR EMBL:AF336562; FT NON-TER ; SQ SEQUENCE 10 AA; 901 MW; 22DF477DD87EASBB CRC64; Query Match Score 22; DB 6; Length 16; Best Local Similarity 75.0%; Pred. No. 4e+03; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RESULT 13 C03604 PRELIMINARY; PRT; 15 AA. ID C03604; PRELIMINARY; PRT; 15 AA. AC 01-JUL-1997 ("TREMBrel": 04, Created) DT 01-JUL-1997 ("TREMBrel": 04, Last sequence update) DT 01-YAR-2001 ("TREMBrel": 05, Last annotation update) DE Type I collagen alpha 1(2) chain (Fragment). GN Homo sapiens (Human). CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; RN 1; RP SEQUENCE FROM N.A.; RX MEDLINE=96316021; Pubmed=8757037; RA Mayer S.A.; Rubin B.S.; Starman B.J.; Byers P.H.; RT "Spontaneous multivessel cervical artery dissection in a patient with RT a substitution of alanine for glycine (G13A) in the alpha 1 (I) chain RT of type I collagen"; RL Neurology 47:552-556(1996). DR EMBL: SB833:5; AACB50780; 2; -. KW Collagen. PT NON-TER 1 1 PT NON-TER 15 15 SQ SEQUENCE 15 AA; 14:3 MW; 4CA8D720AAF780FC CRC64;
Qy	6 GNCG 9 : 3 GSCG 6	RESULT 11 Q95770 PRELIMINARY; PRT; 15 AA. ID Q95770; PRELIMINARY; PRT; 15 AA. AC 01-FEB-1997 ("TREMBrel": 02, Created); DT 01-FEB-1997 ("TREMBrel": 02, Last sequence update) DT 01-DEC-2001 (TREMBrel: 19, Last annotation update) DE NADH dehydrogenase subunit 4 (Fragment). GN Cyclura ricordii. OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Leiosauria; Squamata; Iguania; Iguanidae; Iguaninae; OC Cyclura. NCBI_TaxID=51215; RN 11; RP SEQUENCE FROM N.A.; RX MEJ-NEB197019047; Pubmed=8855662; RA Sires J.W. Jr.; Davis S.K.; Guerra T.; Iverson C.B.; Snell H.L.; PT "Character congruence and phylogenetic signal in molecular and RT morphological data sets: a case study in the living Iguanas (Squamata, RT Iguanidae)"; RT Mol. Biol. Evol. 13:1087-1105(1996). DR EMBL: U66237; AACB50780; 2; -. KW Mitochondrion. PT NON-TER 1 1 PT NON-TER 15 15 SQ SEQUENCE 15 AA; 1715 MW; 8127178E7927A57E CRC64;	Query Match Score 22; DB 6; Length 15; Best Local Similarity 50.0%; Pred. No. 6e+03; Matches 2; Mismatches 2; Indels 0; Gaps 0;
Qy	10 LYYS 13 : : 2 NCLHSTS 9	Query Match Score 22; DB 6; Length 15; Best Local Similarity 50.0%; Pred. No. 4.4e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 7 NCGLYSS 14 : 2 NCLHSTS 9

Best Local Similarity 57.1%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 3; Index's 0;
Gaps 0;

Qy	3	YPSGNCG	9
	4		
Db	4	YICGZCG	10

Search completed: November 5, 2003, 16:58:37
Job time : 36 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model:

Run on: November 5, 2003, 16:48:21 ; Search time: 41 Seconds
(without alignment); 59.071 Million cel. updates/sec

Title: US-09-902-563-18

Perfect score: 88 ; DRYPSGRGGLYSSG ; 15 Sequence: 1107863 seqs, 158726573 residues

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 350435

Minimum DB seq length: 6 Maximum DB seq length: 15

Post-processing: Minimum Match: 100% Maximum Match: 100%

Listing first 45 summaries

Database : A_Geneseq_15Jun03.*

1: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1981.DAT.*
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23: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	88	100.0	15	20 NAW88237	Human prothrombin
2	37	42.0	14	23 AA28619	Human α -beta pro
3	33	37.5	9	22 AAC22853	Human NHC Class I
4	33	37.5	9	22 AAC24113	Human NHC Class II
5	33	37.5	9	22 AAC24423	Human NHC molecule
6	33	37.5	9	22 AAC24441	Human NHC molecule
7	33	37.5	10	22 AAC24481	Human NHC molecule
8	33	37.5	12	22 AAB26044	Human 9E C-epitope
9	33	37.5	12	22 AAU16769	Peptide EED16/47/4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
AAW88237 ID AAW88237 standard; Peptide: 15 AA.
XX DT 15-MAR-1999 (first entry)
XX DE Human prothrombinase Fgl2 epitope.

XX PR 1C-OCT-1997; 97JUS-0061684.
XX PR 15-MAY-1997; 97JUS-0046537.
XX PA LEVY G.
XX PI Levy G.
XX DR WF: 1999-059687/05.
XX PT Modulating immune coagulation. - by using IgG2 antibodies and

EN	W09851335-A1.
XX	19-NCV-1998.
XX	15-MAY-1998; 98WOC-CA00475.
PD	19-NCV-1998.
XX	15-MAY-1997; 97JUS-0061684.

useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 103P2D6-related protein, and a ribozyme capable of cleaving a polynucleotide having the 103P2D6 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 103P2D6. The sequences can be used in diagnostic methods to monitor the level of 103P2D6 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

XX Sequence 9 AA;

Query Match 37.5%; Score 33; DB 22; Length 9;

Best Local Similarity 75.0%; Pred. No. 9.3e-05; Gaps 0;

Matches 6; Conservative 0; Mismatches 2; Indels 0;

Sequence 9 AA;

SQ

5 SGNCGLYY 12

2 SRGRCSGGY 9

RESULT 4

AAU24319

ZD AAU24319 standard; Peptide; 9 AA.

XX

AAU24319;

AC

DT 17-DEC-2001; (first entry)

XX

DE Human YHC class I molecule HLA-B7 binding 103P2D6 peptide #4.

XX

CC cancerous cells.

XX Sequence 9 AA;

SQ Query Match 37.5%; Score 33; DB 22; Length 9;

Best Local Similarity 75.C%; Pred. No. 9.3e+05; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC

CC useful for diagnosing and treating cancer. A vector comprising a

CC polynucleotide which encodes a single chain monoclonal antibody, that

CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme

CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,

CC are both useful in the preparation of a composition for treating a

CC patient with a cancer that expresses 103P2D6. The sequences can be used

CC in diagnostic methods to monitor the level of 103P2D6 gene products in

CC serum, blood, urine and tissue and to thereby detect the presence of

CC cancerous cells.

XX Sequence 9 AA;

SQ Query Match 37.5%; Score 33; DB 22; Length 9;

Best Local Similarity 75.C%; Pred. No. 9.3e+05; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC

CC useful for diagnosing and treating cancer. A vector comprising a

CC polynucleotide which encodes a single chain monoclonal antibody, that

CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme

CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,

CC are both useful in the preparation of a composition for treating a

CC patient with a cancer that expresses 103P2D6. The sequences can be used

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CC serum, blood, urine and tissue and to thereby detect the presence of

CC cancerous cells.

XX Sequence 9 AA;

SQ Query Match 37.5%; Score 33; DB 22; Length 9;

Best Local Similarity 75.C%; Pred. No. 9.3e+05; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC

CC useful for diagnosing and treating cancer. A vector comprising a

CC polynucleotide which encodes a single chain monoclonal antibody, that

CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme

CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,

CC are both useful in the preparation of a composition for treating a

CC patient with a cancer that expresses 103P2D6. The sequences can be used

CC in diagnostic methods to monitor the level of 103P2D6 gene products in

CC serum, blood, urine and tissue and to thereby detect the presence of

CC cancerous cells.

XX Sequence 9 AA;

SQ Query Match 37.5%; Score 33; DB 22; Length 9;

Best Local Similarity 75.C%; Pred. No. 9.3e+05; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC

KW allergic disease; immunoprophylaxis; immunotherapy; antiallergic;
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;
 KW allergy; atopy.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO20050460-A1.
 XX PD 31-AUG-2001.
 XX PF 22-FEB-2000; 2000WO-EP01455.
 XX PR 25-FEB-1999; 99GB-00C4405.
 PR 29-MAR-1999; 99GB-00C7151.
 PR 07-MAY-1999; 99GB-0010537.
 PR 07-MAY-1999; 99GB-0013538.
 PR 07-AUG-1999; 99GB-0018594.
 PR 07-AUG-1999; 99GB-0018603.
 PR 07-SEP-1999; 99GB-0021046.
 PR 29-OCT-1999; 99GB-0022047.
 PR 23-NOV-1999; 99GB-0025619.
 PR 23-NOV-1999; 99GB-0027695.
 XX (SMK) SMMTHKLINE BEECHAM BIOLOGICALS.
 PA (PEP-1) PEPTIDE THERAPEUTICS LTD.
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Jamon A, Mason S,
 PI Randall R, Turnell WG, Van Nechelen MP, Vinals de Bassois YC,
 XX DR WPI; 2000-572073/53.
 XX PT Peptides useful for treating, preventing and ameliorating allergic
 PT diseases, comprising an isolated surface exposed group of a specific
 PT domain from immunoglobulin E -
 XX PS Example 7; Page 53; 129pp; English.
 XX The present invention describes a peptide 'I', comprising an isolated
 CC surface exposed group/epitope '(I)', of C₂-C-epitope 2-domain (CD) of
 CC immunoglobulin E (IgE), or its mimotope. A so described are: (1) an
 CC immunogen '(II)' for treating allergic comprising '(II)': (2) a vaccine ('III');
 CC for treating allergies comprising '(II)': (3) a ligand ('IV') capable of
 CC recognising E; (4) pharmaceutical composition ('PC') comprising ('IV');
 CC (5) a peptide ('ta') capable of being recognised by ('IV'); (6) an immunogen
 CC ('ta') comprising ('ta'); and (7) producing ('III') by producing ('II'). ('
 CC can have anti-allergic and immunosuppressive activities, and can be used
 CC as a vaccine and histamine release inhibitor. ('I'), ('II') and ('III') are
 CC useful in medicine and in the manufacture of medicaments for treating
 CC and preventing allergies. ('IV') is useful for identifying mimotopes of 'I',
 CC in medicine, and also in manufacturing medicaments for treating
 CC allergies. ('I') is also useful in diagnostics and in the affinity purification
 CC of circulating anti-IgE antibodies from blood. ('I'), ('III') and 'PC' are
 CC useful for treating a patient susceptible to or suffering from allergies.
 CC Peptide sequences which are used in the exemplification of the present
 CC invention.
 XX SQ Sequence 12 AA:
 XX Query Match Similarity 37.5%; Score 33; DB 21; Length 12;
 CC Best Local Similarity 83.3%; Pred. No. 2e+02; Mismatches 1; Indels 0; Gaps 0;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC Cy 4 PSGNCG 9
 CC Dib 4 PGGDCCG 9

RESULT 9
 AAU16769
 ID AAB16769 standard; Peptide, 12 AA.
 XX AC AAU16769;

XX DT 07-NOV-2001 (first entry)
 XX DE Peptide EED18/47/48 derived from Cepsiion2 region of human IgE.
 XX Human linkage technology; conjugated compound; carrier vehicle;
 KW epitope; Cepsiion2; Cepsiion3; Cepsiion4; immunoglobulin E;
 KW IgE mediated disease; antibody response.
 XX OS Homo sapiens.
 CS Synthetic.
 XX FN WC2C0-45745-A2.
 XX FD 28-JUN-2001.
 XX PF 21-DEC-2000; 2000WO-GB04935.
 XX PR 21-DEC-1999; 99GB-0C30233.
 PR 22-FEB-2000; 2000GB-0CC4096.
 PR 22-AUG-2000; 2000GB-0J20137.
 PR 22-AUG-2000; 2000GB-0020708.
 XX 'ACAMBIS RES LTD.
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX Example 4; Page 23; 4app; English.
 XX The present invention relates to linkage methodology for use in the
 CC conjugation of compounds (e.g. peptides) to carrier vehicles
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce
 biological and immunological constructs. The invention provides a
 CC method for linking an epitope (e.g. a peptide), to a carrier (e.g. a
 protein); for use in a pharmaceutical composition or a vaccine. The
 CC invention describes peptides derived from or mimotopes of the
 Cepsiion2, Cepsiion3 or Cepsiion4 regions of human immunoglobulin E
 (IgE) which are used to produce conjugated compounds. The compounds or
 CC compositions of the invention are useful in the manufacture of a
 CC medicament for the treatment of IgE mediated diseases. The invention
 CC allows for controlled conjugation of a peptide epitope (antigen) to a
 CC protein so as to form an immunogenic conjugate which may be able to
 CC raise a protective antibody response in an animal or human patient.
 CC AAU1662-AAU16913 represent peptides derived from or mimotopes of
 CC the Cepsiion2/Cepsiion3/Cepsiion4 region of human IgE.
 XX SQ Sequence 12 AA:
 XX Query Match Similarity 37.5%; Score 33; DB 22; Length 12;
 CC Best Local Similarity 83.3%; Pred. No. 2e+02; Mismatches 1; Indels 0; Gaps 0;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC Cy 4 PSGNCG 9
 CC Dib 4 PGGDCCG 9

RESULT 10
 AB-00390
 ID ABJ00390 standard; Peptide, 12 AA.
 XX AC AEJ00390;
 XX DT 02-SEP-2002 (first entry)
 XX DE Human IgE cyclic immunogenic peptide SEQ ID NO: 174.

KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;
 KW vaccine; antiallergic; cyclic.

XX Homo sapiens.

XX NC200216409-A2.

PD 28-FEB-2002.

XX 17-AUG-2001; 2001WO-FP209576.
 PR 22-AUG-2001; 2000GB-0020717.

XX (SMIK) SMITHKLINE BEPHAM BIOLOGICALS.
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.

XX Friede M, Mason S, Turnell MG, Vinalis Bassols YC;

XX WPI; 2002-489648/52.

XX Conjugate for use in vaccine for treatment of allergy; comprises
 PT disulfide bridge cyclized peptide and immunogenic carrier -
 PT claim 4; Page 13; 45pp; English.

XX The present invention relates to conjugates suitable for use in vaccines,
 CC where the conjugate comprises a disulfide bridge cyclised peptide and an
 CC immunogenic carrier. The vaccines can be used in the treatment of
 CC arteries. The present sequence is a cyclic peptide immunogen derived
 CC from human immunoglobulin E (IgE) suitable for use in the invention.

XX Sequence 12 AA:

Query Match Score 33; DB 23; Length: 12;
 Best Local Similarity Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PGGNCG 9
 Db 4 PGGDCG 9

RESULT 11
 ID AAW23509 standard; Peptide: 15 AA.
 XX AAW23509;
 AC AAW23509;

XX 18-SEP-1997 (first entry)

DE Purified cis-9,10-octadecenoamidase internal amino acid fragment.
 XX Coase; cis-9,10-octadecenoamidase; oleic acid; catalysis;
 KW affinity chromatography; electric chromatography;
 KW gel filtration chromatography; ion exchange chromatography;
 KW partition chromatography; fatty acid primary amide; sleep-inducing;
 KW inhibitor; specific; rat.

XX Rattus ratus.

XX WC9641869-A1.
 PR 12-JUN-1995; 95US-0489535.
 PA (SCRI) SCRIPPS RES INST.

XX Cravatt BF, Gilula NB, Lerner RA;

XX DR 12-JUN-1995; 96WO-US10435.

XX PS 12-JUN-1995; 95US-0489535.

XX PA (SCRI) SCRIPPS RES INST.

XX Cravatt BF, Gilula NB, Lerner RA;

DR WPI; 1997-065456/06.

XX Purified cis-9,10-octadecenoamidase (Coase) has been
 PT sleep-inducing fatty acid primary amide(s), and identifying
 PT inhibitors

XX PS Claim 1; Page 78; 101pp; English.

XX A purified form of cis-9,10-octadecenoamidase (Coase) has been
 CC obtained by a chromatographic methodology selected from affinity,
 CC electric, gel filtration, ion exchange and partition chromatography.
 CC The Coase is characterised by enzymic activity for catalysing the
 CC conversion of cis-9,10-octadecenoamide (CO) to oleic acid and by the
 CC inclusion of an amino acid sequence fragment from rat liver Coase.
 CC The present sequence represents a specifically claimed example of such
 CC an amino acid fragment. This fragment is found at residues 31 to 45 of
 CC rat liver Coase as shown in AAW0465. The Coase can be used to catalyse
 CC the hydrolysis of fatty acid primary amides, which have sleep-inducing
 CC activity. The Coase can also be used to identify inhibitors of the
 CC Coase activity.

XX SQ Sequence 15 AA;

Query Match Score 33; DB 18; Length 15;
 Best Local Similarity Pred. No. 2.5e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0; C;
 Qy 2 RYSGNCGL 1C
 ||| :||:
 Db 1 RPPSAFCG 9

RESULT 12

AAW57788 standard; Peptide: 15 AA.

ID AAW57788

XX AC AAW57788;

DT 12-OCT-1998 (first entry)

XX DF Fatty acid amide hydrolase Peptide (e).

XX KW Cis-9,10-octadecenoamidase; fatty acid amide hydrolase; FAAH;

CC clamidase hydrolase; soporitic; sleep.

XX Mammalia.

XX WC820119-A1.

XX 14-NAY-1998.

XX FF 04-NOV-1997; 97WO-US20365.

XX PR 04-NOV-1996; 96US-C743168.

XX PA (SCRI) SCRIPPS RES INST.

XX Cravatt BF, Gilula NB, Lerner RA;

XX WPI; 1998-286935/25.

XX New fatty acid amide hydrolases (FAAHs) of the invention are
 PT characterised by inclusion of an amino acid sequence selected from
 CC a group of 28 sequences (see AAW57784-811). These FAAHs can hydrolyse
 CC cis-9,10-octadecenoamide, anandamide (arachidoyl ethanolamine), and
 CC myristic, palmitic or stearic amides. Also new are: (1) inhibiting
 CC hydrolysis of fatty acid primary amides catalysed by FAAH by
 CC treatment with an FAAH inhibitor; (2) a method of screening for an

CC FAAH inhibitor; (3) the FAAH inhibitor of formula
 CC CF₃CC(CH₂)₇-CH₂CH(cis)- (CH₂)₇Mel; and (4) nucleic acid encoding FAAH
 CC or parts of it. FAAH catalyzes conversion of fatty acid primary
 CC amides, particularly those in which the alkyl group has a cis
 CC unsaturation. These amides induce sleep, so FAAH can be used to
 CC study processes in which they are involved and also to develop
 CC agents for modulating sleep.

XX SQ Sequence 15 AA;

Query Match Score 33; DB 19; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2.5e-02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RYPSGNGL 10
 Db 1 RFPSAFCGI 9

RESULT 13

AGG9214 AGG9214 standard; Peptide; 10 AA.
 ID XX
 AC AGG9214;
 XX
 XX -8-SEP-2001 (first entry)

XX Human complementary peptide, SEQ ID NO: 2408.
 XX Human; complementary peptide; ligand; drug discovery; drug design.
 OS Homo sapiens.
 XX PN WO200142277-A2.
 XX PD 14-JUN-2001.
 XX FF 13-DEC-2005; 20000WC-GB04776.
 XX PR 13-DEC-1999; 99GB-C029464.
 XX PA (PROT-) PROTEOM LTD.
 XX PI Roberts GM, Heai JR;
 XX DR 2001-40849/4j.
 XX PT A set of peptide ligands consisting of specific complementary peptides
 PT to proteins encoded by genes of the human genome, useful in an assay
 PT for screening and generation of one or more novel peptides which are
 PT drug candidates or pro-drugs -
 XX Example 4; Page 386; 646pp; English.
 XX The invention relates to a set of complementary peptide ligands
 CC generated from the human genome. The complementary peptides
 CC interact with their relevant target proteins encoded in the human
 CC genome. They can be used as reagents in drug discovery and as lead
 CC ligands to facilitate drug design and development. The present
 CC sequence is a complementary peptide provided in the specification.
 XX SQ Sequence 10 AA;

Query Match Score 31; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SCNCG 9
 Db 6 SCNCG 10

RESULT 14

AAF4C32B
 ID AAF4C32B standard; Peptide; 15 AA.
 XX
 XX AAF4032B;
 AC
 XX 16-AUG-2C02 (updated)
 DT 30-JAN-1992 (first entry)
 XX
 Sequence of conotoxin peptide GIA.
 XX Acetylcholine receptor; reversible immobilisation;
 KW synaptic transmission inhibitor.
 XX
 Corus Geographus.
 CS Synthetic.
 XX
 Key 2.7
 PT Disulfide-bond 3
 PT Modified-site /label= Cys-S-(acetamido-methyl)
 PT Modified-site 13
 PT /label= Cys-S-(acetamido-methyl)
 PT Modified site 15
 PT /label= Lys-NH₂
 XX US447156-A.
 XX 08-MAY-1984.
 XX 04-JUN-1982; 82US-0365125.
 XX 04-JUN-1982; 82US-0365125.
 PR 17-APR-1981; 81US-0255237.
 XX PA ;OLIV/; OLIVERA B M.
 XX
 XX Olivera BM, Cruz LC, Gray WR, Rivier JEP;
 DR 1984-133757/2.
 XX Conotoxin peptide(s) - useful for reversible immobilisation of
 PT muscles and for detecting acetyl:choline receptors
 XX
 XX Claim 5; column 2; 10pp; English.
 XX
 The peptides of the invention are potent inhibitors of synaptic
 CC transmission at the neuromuscular junction while lacking inhibition
 CC of either nerve or muscle action potential propagation. Their action
 CC is freely reversible on dilution or removal of the peptides from the
 CC affected muscle. The peptides are useful for reversible
 CC immobilisation of a muscle or gp. of muscles in man and other
 CC vertebrates and they can be used for detection and measurement of
 CC acetylcholine receptors.
 CC
 XX Sequence 15 AA;
 CC
 CC The peptides of the invention are potent inhibitors of synaptic
 CC transmission at the neuromuscular junction while lacking inhibition
 CC of either nerve or muscle action potential propagation. Their action
 CC is freely reversible on dilution or removal of the peptides from the
 CC affected muscle. The peptides are useful for reversible
 CC immobilisation of a muscle or gp. of muscles in man and other
 CC vertebrates and they can be used for detection and measurement of
 CC acetylcholine receptors.
 CC
 XX
 XX Query Match Score 35.2%; Score 31; DB 5; Length 15;
 CC Best Local Similarity 62.5%; Pred. No. 4.9e+02;
 CC Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC
 Qy 8 CGLYYSSG 15
 Db 7 CCRHYSSG 14

RESULT 15

ARR75265
 ID ARR75265 standard; Peptide; 15 AA.
 AC
 XX
 AC ARR75265;
 XX
 DT 21-DEC-1995 (first entry)

XX Alpha-conotoxin: GIA peptide.
 DE XX
 KW Alpha conotoxin; inhibit; neuromuscular; synapse; signal transmission.
 XX
 OS Conus geographus.
 XX PN W09511256-A.
 XX
 PC 27-APR-1995.
 XX PF 19-OCT-1994; 94WO-US11927.
 XX PR 19-OCT-1993; 93US-0137900.
 XX PA UTAH) UNIV UTAH RES FOND.
 XX PI Cruz LJ, Hilliard DR, McIntosh JM, Oliviera SM, Santos AD;
 XX WPI: 1995-170189/22.

XX New A-lineage conotoxin peptide(s) - which inhibit synaptic
 PT transmission at the neuromuscular junction or are active against
 PT potassium or sodium channels
 XX Disclosure: Page 4; 66pp; English.
 XX The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin
 CC peptides all belong to a group of Peptides known as the A-lineage
 CC conotoxin Peptides. The A-lineage Conotoxin Peptides have a wide
 CC variety of pharmacological uses. The A-lineage Conotoxin Peptides
 CC claimed (AR75264-R75293) are useful for the inhibition of synaptic
 CC transmission at neuromuscular junctions by blocking nicotinic acetyl
 CC choline receptors and they also have activity against voltage-gated Na
 CC channels.
 XX Sequence 15 AA;

Query Match 35.2%; Score 31; DB 16; Length 15;
 Best Local Similarity 62.5%; Pred. No. 4 9e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 8 CGLYSSG 15
 25 7 CORHYSCS 24

Search completed: November 5, 2003. 16:57:26
 Job time : 42 secs

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CM protein - protein search, using SW model

Run on: November 5, 2003, 16:58:41 ; Search time 28 Seconds

(without alignments)
92,009 Million cell updates/secTitle: JS-09-902-563-18
Perfect score: 86
Sequence: 1 DRYPSGNGLYSSG 15Scoring table: BLASTM52
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 17,749,292 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 3

Maximum DB seq length: 15

Post-processing: Minimum Watch 0%

Maximum Watch 100%

Listing first 45 summaries

Database : Published Applications AA: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description:
1	88	100.0	15	11	US-09-902-563-18
2	88	100.0	15	15	US-10-096-255-18
3	37	42.0	14	15	US-10-056-884-11
4	35	39.8	10	9	US-10-819-308-25
5	33	37.5	9	12	US-09-733-451-52
6	33	37.5	9	12	US-09-733-451-518
7	33	37.5	9	12	US-09-733-451-622
8	33	37.5	9	12	US-09-733-451-640
9	33	37.5	9	12	US-10-283-722-52
10	33	37.5	9	12	US-10-283-722-518
11	33	37.5	9	12	US-10-283-722-622
12	33	37.5	9	12	US-10-283-722-640
13	33	37.5	10	12	US-09-733-451-683
14	33	37.5	10	12	US-10-283-722-683
15	35.2	33.0	10	12	US-09-733-451-52

RESULT 1
US-C9-902-563-18
; Sequence 18, Application US-099C2563
; Publication No. US2003096541
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT FILING DATE: 2002-09-09
; PRIORITY APPLICATION NUMBER: US 09/902,563
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO: 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-902-563-18

Query Match 100.0%; Score 88; DB 1.; Length 15
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 DRYPSGNGLYSSG 15
Db 1 DRYPSGNGLYSSG 15
RESULT 2
US-10-036-255-18
; Sequence 18, Application US-10096255
; Publication No. US20030103974A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Clark, David A.
; FILE REFERENCE: 9579-52

CURRENT APPLICATION NUMBER: US/10/096,255
 CURRENT FILING DATE: 2002-03-13
 PRIOR APPLICATION NUMBER: US 60/046,537
 PRIOR FILING DATE: 1997-05-17
 PRIORITY NUMBER: US 60/061,684
 PRIORITY FILING DATE: 1997-10-10
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 18
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-096-255-18

Query Match Score 92; DB 15; Length 15;
 Best Loca. Similarity 100.0%; Pred. No. 4.9e-01;
 Xmatches 0; Indels 0; Gaps 0;

Qy 1 DRPSGNGLYSSG 15
 Db 1 DRPSGNGLYSSG 15

RESULT 3
 JS-10-056-884-11
 Sequence 11: Application US/10056884
 Publication No. US20030012796A1
 GENERAL INFORMATION:
 APPLICANT: Bristol Myers Squibb Company
 TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT INVENTION: K-betam2
 FILE REFERENCE: D0076_NP
 CURRENT APPLICATION NUMBER: US/10/056,884
 CURRENT FILING DATE: 2002-01-24
 PRIOR APPLICATION NUMBER: US 60/263,872
 PRIOR FILING DATE: 2001-01-24
 PRIOR APPLICATION NUMBER: US 60/269,794
 PRIOR FILING DATE: 2001-02-14
 NUMBER OF SEQ ID NOS: 73
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 12
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-056-884-11

Query Match Score 37; DB 15; Length 14;
 Best Loca. Similarity 42.0%; Pred. No. 3.1;
 Xmatches 0; Indels 0; Gaps 0;

Qy 5 SGNGLYY 12
 Db 4 SGNCRRYY 11

RESULT 4
 JS-09-819-308-25
 Sequence 25: Application JS/09819308A1
 GENERAL INFORMATION:
 APPLICANT: No. US2002018040A1
 APPLICANT: Danen-van Cosschot, Astrid
 APPLICANT: Roht, Jennifer
 FILE REFERENCE: 2906-4820US
 CURRENT APPLICATION NUMBER: US/09/819,308
 CURRENT FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 25
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Sequence homology analysis of AAP-5

US-09-819-308-25
 Query Match Score 35; DB 9; Length 10;
 Best Loca. Similarity 85.7%; Pred. No. 4.6;
 Xmatches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CGTYYSS 14
 Db 3 CGTYYSS 9

RESULT 5
 JS-09-793-451-52
 Sequence 52: Application US/09793451
 Publication No. US2003015597A1
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Ed
 APPLICANT: Mary Paris
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY EXPRESSED IN VARIOUS CANCERS
 FILE REFERENCE: 129_2USU2
 CURRENT APPLICATION NUMBER: US/09/793,451
 CURRENT FILING DATE: 2001-02-26
 PRIOR APPLICATION NUMBER: 60/184,558
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/218,856
 PRIOR FILING DATE: 2000-07-13
 NUMBER OF SEQ ID NOS: 752
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 52
 LENGTH: 9
 TYPE: PRT
 ORGANISM: homo sapiens
 JS-09-793-451-52

Query Match Score 33; DB 12; Length 9;
 Best Loca. Similarity 75.0%; Pred. No. 5.8e+05;
 Xmatches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 SGNGLYY 12
 Db 2 SGRCGLY 9

RESULT 6
 JS-09-793-451-518
 Sequence 518: Application JS/09793451
 Publication No. US2003015597A1
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Ed
 APPLICANT: Mary Paris
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY EXPRESSED IN VARIOUS CANCERS
 FILE REFERENCE: 129_2USU2
 CURRENT APPLICATION NUMBER: US/09/793,451
 CURRENT FILING DATE: 2001-02-26
 PRIOR APPLICATION NUMBER: 60/184,558
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/218,856
 PRIOR FILING DATE: 2000-07-13
 NUMBER OF SEQ ID NOS: 752

SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 518
 LENGTH: 9
 TYPE: PRT
 ORGANISM: homo sapiens
 US-09-793-451-518

Query Match:
 Best Local Similarity 75.0%; Score 33; DB 12; Length 9;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 TYPE: PRT
 ORGANISM: homo sapiens
 JS-09-793-451-640

Query Match:
 Best Local Similarity 75.0%; Score 33; DB 12; Length 9;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 JS-09-793-451-640

Query Match:
 Best Local Similarity 75.0%; Score 33; DB 12; Length 9;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 JS-09-793-451-640

RESULT 7
 US-09-793-451-622
 Sequence 622, Application US/C9793451
 Publication No. US20030157537A1
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Gazelle S. Rastegar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Mary Paris
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 103P226: TISSUE SPECIFIC PROTEIN HIGHLY
 TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
 FILE REFERENCE: 129.ZUSU2
 CURRENT APPLICATION NUMBER: US/09/793,451
 CURRENT FILING DATE: 2001-02-26
 PRIOR APPLICATION NUMBER: 60/1184,558
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/218,856
 PRIOR FILING DATE: 2000-07-13
 NUMBER OF SEQ ID NCS: 752
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 622
 LENGTH: 9
 TYPE: PRT
 ORGANISM: homo sapiens
 US-09-793-451-622

Query Match:
 Best Local Similarity 75.0%; Score 33; DB 12; Length 9;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 TYPE: PRT
 ORGANISM: homo sapiens
 JS-09-793-451-622

Query Match:
 Best Local Similarity 75.0%; Score 33; DB 12; Length 9;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 JS-09-793-451-622

RESULT 8
 US-09-793-451-640
 Sequence 640, Application US/C9793451
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Gazelle S. Rastegar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Eid

RESULT 9
 JS-10-283-722-52
 Sequence 52, Application US/10283722
 Publication No. US20030194407A1
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Gazelle S. Rastegar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Mary Paris
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
 EXPRESSED IN VARIOUS CANCERS
 FILE REFERENCE: 129.ZUSU2
 CURRENT APPLICATION NUMBER: US/10/283,722
 CURRENT FILING DATE: 2003-02-03
 PRIOR APPLICATION NUMBER: US/09/793,451
 PRIOR FILING DATE: 2001-02-25
 PRIOR APPLICATION NUMBER: 60/1184,558
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/218,856
 PRIOR FILING DATE: 2000-07-13
 NUMBER OF SEQ ID NOS: 752
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 52
 LENGTH: 9
 TYPE: PRT
 ORGANISM: homo sapiens
 JS-10-283-722-52

Query Match:
 Best Local Similarity 75.0%; Score 33; DB 12; Length 9;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 JS-10-283-722-52

RESULT 10
 JS-10-283-722-518
 Sequence 518, Application US/10283722
 Publication No. US20030194407A1
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Gazelle S. Rastegar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Eid

RESULT 11
 JS-10-283-722-512
 Sequence 512, Application US/10283722
 Publication No. US20030194407A1
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Gazelle S. Rastegar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Eid

APPLICANT: Mary Faris
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 13P256: TISSUE SPECIFIC PROTEIN HIGHLY
 EXPRESSED IN VARIOUS CANCERS
 FILE REFERENCE: 129 2USU2
 CURRENT APPLICATION NUMBER: US/10/283,722
 PRIOR APPLICATION NUMBER: US/09/793,451
 PRIOR FILING DATE: 2001-02-26
 PRIOR APPLICATION NUMBER: 60/184,558
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/218,956
 PRIOR FILING DATE: 2000-07-13
 NUMBER OF SEQ ID NOS: 752
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 518
 LENGTH: 9
 TYPE: PRT
 ORGANISM: homo sapiens
 JS-10-283-722-518

Query Match 37.5%; Score 33; DB 12; Length 9;
 Best Local Similarity 75.0%; Pred. No. 5.8e+05;
 Matches 6; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;

Qy 5 SGNCGLYY 12
 Db 1 SGRCGLGY 8

RESULT 12
 US-10-283-722-622
 Sequence 622, Application US/10/283,722
 Publication No. US2003019447A.
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Gazelle S. Rastegar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Mary Faris
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 13P256: TISSUE SPECIFIC PROTEIN HIGHLY
 EXPRESSED IN VARIOUS CANCERS
 FILE REFERENCE: 129 2USU2
 CURRENT APPLICATION NUMBER: US/10/283,722
 PRIOR FILING DATE: 2001-02-03
 PRIOR APPLICATION NUMBER: US/09/793,451
 PRIOR FILING DATE: 2000-02-26
 PRIOR APPLICATION NUMBER: 60/184,558
 PRIOR FILING DATE: 2000-07-13
 PRIOR APPLICATION NUMBER: 60/218,856
 PRIOR FILING DATE: 2000-07-13
 NUMBER OF SEQ ID NOS: 752
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 622
 LENGTH: 9
 TYPE: PRT
 ORGANISM: homo sapiens
 JS-10-283-722-622

Query Match 37.5%; Score 33; DB 12; Length 9;
 Best Local Similarity 75.0%; Pred. No. 5.8e+05;
 Matches 6; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;

Qy 5 SGNCGLYY 12
 Db 2 SGRCGLGY 9

RESULT 12
 US-10-283-722-640

Qy 5 SGNCGLYY 12
 Db 2 SGRCGLY 9

RESULT 14
 US-10-283-722-683
 / Sequence 683; Application US/10283722
 / GENERAL INFORMATION:
 / Publication No. US20030194407A.
 / APPLICANT: Arthur B. Raitano
 / APPLICANT: Daniel E.H. Afr
 / APPLICANT: Gazelle S. Rasegar
 / APPLICANT: Steve Chappell Mitchell
 / APPLICANT: Rene S. Hubert
 / APPLICANT: Pia M. Chalita-Bid
 / APPLICANT: Aya Jakobovits
 / TITLE OF INVENTION: 10P226: TISSUE SPECIFIC PROTEIN HIGHLY
 / FILE REFERENCE: 129 2USU2
 / CURRENT APPLICATION NUMBER: US112/293,722
 / CURRENT FILING DATE: 2003-02-03
 / PRIOR APPLICATION NUMBER: US/09/793,451
 / PRIOR FILING DATE: 2001-02-26
 / PRIOR APPLICATION NUMBER: 60/184,558
 / PRIOR FILING DATE: 2000-02-24
 / PRIOR APPLICATION NUMBER: 60/218,856
 / PRIOR FILING DATE: 2000-01-13
 / NUMBER OF SEQ ID NCS: 752
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO: 683
 / LENGTH: 10
 / TYPE: PRT
 / ORGANISM: homo sapiens
 US-10-283-722-683

Query Match Score 33; DB 12; Length 10;
 Best Local Similarity 75.0%; Pred. No. 93;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 SGNCGLYY 12
 Db 2 SGRCGLY 9

RESULT 15
 US-09-572-404B-2408
 / Sequence 2408; Application US/09572404B
 / Publication No. US2003078374A1
 / GENERAL INFORMATION:
 / APPLICANT: Proteam Lrd
 / TITLE OF INVENTION: Complementary Peptide ligands from the human genome
 / CURRENT APPLICATION NUMBER: US/09/572,404B
 / CURRENT FILING DATE: 2000-05-17
 / NUMBER OF SEQ ID NOS: 4203
 / SOFTWARE: Proteam version 1.0
 / SEQ ID NC 2408
 / LENGTH: 10
 / TYPE: PRT
 / ORGANISM: Homo Sapiens
 / FEATURE:
 / OTHER INFORMATION: sequence located in GATA1 OR GFI OR ERYF1 at 336-347 and may interact
 / OTHER INFORMATION: with Sequence 2407 in this patent.
 US-09-572-404B-2408

Query Match Score 31; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1,98-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SGNCGLYY 9
 :|||:

RESULT 4
JS-08-137-800-5
Sequence 5, Application US/C81178C0
Patent No. 5514774

GENERAL INFORMATION:
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Hillyard, David R.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Santos, Amurfiro M.
 TITLE OF INVENTION: Conotoxin Peptides
 NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue N.W., Suite 1000
 CITY: Washington
 STATE: DC
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/489,535
 FILING DATE: 12-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 TELECOMMUNICATION INFORMATION:
 NUMBER: TSR-495.2
 TELEPHONE: (619) 784-2937
 TELEFAX: (619) 744-9199

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: Interna;
 US-08-743-168B-9

Query Match 37.5%; Score 33; DB 3; Length 15;
 Best Local Similarity 55.6%; Pred. No. 70;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RYPGNNGGL 10
 | :| :|| :| :|
 Db 1 RFPSAFCG 9

RESULT 3
PCT-US96-10435-9
Sequence 9, Application PC/TUSS610435

GENERAL INFORMATION:
 APPLICANT: The Scripps Research Institute
 TITLE OF INVENTION: CIS-9, 10-OCTADECENAMIDE
 NUMBER OF SEQUENCES: 32

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #: 25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/0435
 FILING DATE: 12-JUN-1996

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/489,535
 FILING DATE: 12-JUN-1995

SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 FRAGMENT TYPE: Interna;
 PCT-US96-10435-9

Query Match 37.5%; Score 33; DB 5; Length 15;
 Best Local Similarity 55.6%; Pred. No. 70;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RYPGNNGGL 10
 | :| :|| :| :|
 Db 1 RFPSAFCG 9

RESULT 5
US-08-477-383-5
Sequence 5, Application US/08417383
Patent No. 5589340

GENERAL INFORMATION:
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Hillyard, David R.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Santos, Amurfiro S.
 TITLE OF INVENTION: Conotoxin Peptides
 NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: U.S.A.

ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,383
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/117,800
 FILING DATE: 19-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,383
 FILING DATE: 29-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24260-107673
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NC: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 CRITICAL SOURCE:
 ORGANISM: Conus geographus

RESULT 7
 US-08-477-383-5
 Query Match: 35.2%; Score: 31; DB 1; Length: 15;
 Best Local Similarity: 62.5%; Pred. No.: 1.4e+52;
 Matches: 5; Conservative: 1; Mismatches: 2; Indels: 0; Gaps: 0;
 Qy: 8 CGLYSSG 15
 ||| :|||
 Db: 7 GRYHSCG 14

RESULT 7
 US-08-487-174-5
 Query Match: 35.2%; Score: 31; DB 1; Length: 15;
 Best Local Similarity: 62.5%; Pred. No.: 1.4e+52;
 Matches: 5; Conservative: 1; Mismatches: 2; Indels: 0; Gaps: 0;
 Qy: 8 CGLYSSG 15
 ||| :|||
 Db: 7 GRYHSCG 14

RESULT 6
 US-08-487-174-5
 Sequence 5, Application US/38487174
 Patent No. 555972
 GENERAL INFORMATION:
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Cruz, Lourdes C.
 APPLICANT: Macinost, David R.
 APPLICANT: Macinost, J. Michael
 APPLICANT: Santos, Amurino S.
 TITLE OF INVENTION: Conotoxin Peptides
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue, N.W., Suite 1C00
 CITY: Washington
 STATE: DC
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,174
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810

RESULT 9
 US-07-923-724-57
 Sequence 57, Application US/07323724
 GENERAL INFORMATION:
 APPLICANT: Nevalainen, Helena K.M.
 APPLICANT: Palohelmo, Marja T.
 APPLICANT: Miettinen-Oinonen, Arja S.K.
 APPLICANT: Torkki, Tuula K.
 APPLICANT: Cantrell, Michael J.
 APPLICANT: Piddington, Christopher S.
 APPLICANT: Ramboeck, John A.
 APPLICANT: Turunen, Maria K.
 APPLICANT: Pagerström, Richard B.
 TITLE OF INVENTION: Production of Phytase Degradation Enzymes
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESS: Steree, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/C7/923,724
 FILING DATE: 31-JUL-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 37/496,155
 FILING DATE: 19-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/044,077
 FILING DATE: 29-APR-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: UK 8610600
 FILING DATE: 30-APR-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Cimbala, Michelle A.
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 105G.0240004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NC: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Corus geographus
 PCT-US96-07962-2

Query Match 35.2%; Score 31; DB 1; Length 15;
 Best Local Similarity 65.5%; Pred. No. 1.e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
 PCT-US96-07962-2
 Sequence 2, Application PC/TJS9607962
 GENERAL INFORMATION:
 APPLICANT: University of Utah Research Foundation
 TITLE OF INVENTION: Use of Conotoxin Peptides U02 and X-1
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue, N.W., Suite 1003
 CITY: Washington
 STATE: DC
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-WINDOWS
 SOFTWARE: Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/TJS96/07962
 FILING DATE: 04-CIN-1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/448,174
 FILING DATE: 07-JUN-1995
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Corus geographus
 PCT-US96-07962-2

Query Match 35.2%; Score 31; DB 1; Length 15;
 Best Local Similarity 65.5%; Pred. No. 1.e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
 US-07-923-724-57
 Sequence 57, Application US/088C9426A
 GENERAL INFORMATION:
 APPLICANT: Nevalainen, Helena K.M.
 APPLICANT: Palohelmo, Marja T.
 APPLICANT: Miettinen-Oinonen, Arja S.K.

Query Match 34.1%; Score 30; DB 1; Length 13;
 Best Local Similarity 55.6%; Pred. No. 1.e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query 1 DRYPSGNCC 9
 Db 4 ERYPPSGAG 12
 Ds 4 ERYPPSGAG 12

APPLICANT: Torkkeli, Tuula K.
 APPLICANT: Cantrell, Michael
 APPLICANT: Piddington, Christopher S.
 APPLICANT: Rambosek, John A.
 APPLICANT: Turunen, Maria K.
 APPLICANT: Fagerström, Richard B.
 APPLICANT: Houston, Christine S.
 TITLE OF INVENTION: Production of Phytase Degrading Enzymes
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/M-DCS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/CS/609,446A
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/923,724
 FILING DATE: 31-JUL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US C7/426,155
 FILING DATE: 19-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/044,077
 FILING DATE: 29-APR-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: UK 861050
 FILING DATE: 30-APR-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Grant E.
 TELEPHONE: (202) 371-1600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 TOPOLOGY: both
 S-08-609-426A-57

Query Match	Score	DB	Length
Y	34.1%	2;	13;
Y	55.6%	1e+02;	
Y	5.6%	2;	
Y	0.0%	2;	
Y	0.0%	2;	

Mismatches: 2; Indexes: 0

1 DRYPSPGNCG 9
 : : : : : : :
 4 ERYPPSPSAG 12

RESULT 1:
 S-08-374-652C-4
 Sequence 44, Application US/08374652C
 Patent No. 5834286
 GENERAL INFORMATION:
 APPLICANT: NEVALAINEN, HELENA K.M.
 APPLICANT: PALOHIMO, MARJA T.
 APPLICANT: FAGERSTROM, RICHARD B.
 APPLICANT: MATTINEN-OINONEN, ARJA S.
 APPLICANT: TURUNEN, MARIA K.
 APPLICANT: RAMBOSEK, JOHN A.
 APPLICANT: PIDDINGTON, CHRISTOPHER S.

APPlicant: HOUSTON, CHRISTINE S.
 APPlicant: CANTRELL, MICHAEL A.
 TIME OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
 TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
 NUMBER OF SEQUENCES: 944
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STEENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 COMPUTER TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DCS MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/374,652C
 FILING DATE: 24-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/3705B
 FILING DATE: 27-JUL-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 57/925,401
 FILING DATE: 31-JUL-1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: REED, GRANT E.
 REGISTRATION NUMBER: 41,264
 REFERENCE/DOCKET NUMBER: 105C-071CC1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-26CC
 TELEFAX: 202-371-2550
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 US-08-374,652C-44

Query	1 DRYPGNCG 9	DB	4 ERYPPSAG 12	
Query Match	34.1%	Score 3C;	DB 2;	Length 13;
Best Local Similarity	55.6%	Pred. No. 1.7e+02;		
Matches	5;	Mismatches	2;	Indels 0;
				Gaps 0

RESULT 12
 US-08-355-2257A-42
 Sequence 42, Application US/08553257A
 ; Patent No. 5994033
 GENERAL INFORMATION:
 APPlicant: ISTITUTO DI RICERCHE DI BIOLOGIA
 MOLECOLARE P. ANGELETTI S.p.A.
 APPlicant: FELICITÀ, Franco
 APPlicant: LUZZAGO, Alessandra
 APPlicant: NICOSTA, Alfredo
 APPlicant: MONACI, Paolo
 APPlicant: CORTESE, Riccardo
 TIME OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
 TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brody and Neimark

STREET: 419 Seventh Street N.W. Ste. 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release 41.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,257A

FILING DATE: 11-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: RM93A0C030-

FILING DATE: 05-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: FEJ-ZCI=1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEX: (202) 737-3528

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: recombinant protein

HYPOTHETICAL: yes

FRAGMENT TYPE: internal

IMMEDIATE SOURCE:

LIBRARY: of recombinant peptides on phage

CLOSE: phagic

FEATURE: peptide

NAME/KEY: Polypeptide

IDENTIFICATION METHOD: selection with specific antibodies

US-08-553-257A-42

Query Match

Best Local Similarity

Matches

Score 30; DB 2; Length 15;

Pred. No. 2e+02;

Mismatches 0;

Gaps 0;

Indels 0;

Cl:

4 PSGAGG 9

|||

9 FSGAGG 14

RESULT 14

US-08-553-257A-42

Sequence 91, Application US/08432871C

Patent No. 58770-0

GENERAL INFORMATION:

APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA

MOLECOLARE P. ANGELUTTI S.P.A.

FELICI, Franco

LIZZAGO, Alessandra

NICOSIA, Alfredo

MONACI, Paolo

CORTESI, Riccardo

TITLE OF INVENTION:

PROCESS FOR THE PREPARATION OF IMMUNOGENS

OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR

DIAGNOSTIC REAGENTS THEREBY OBTAINABLE

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street N.W. Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: US

Z-P: 981C4-7092

COMPUTER READABLE FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,871C

STATE: D.C.
 COUNTRY: USA
 ZIP: 20044
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,257A
 FILING DATE: 11-MAY-1993
 PRIORITY DATA:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: RM93A0C030-
 FILING DATE: 05-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Browdy, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: FEJ-ZCI=1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 TELEFAX: (202) 737-3528
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: recombinant protein
 FRAGMENT TYPE: internal
 IMMEDIATE SOURCE:
 LIBRARY: of recombinant peptides on phage
 CLOSE: phagic
 FEATURE:
 NAME/KEY: Polypeptide
 IDENTIFICATION METHOD: selection with specific antibodies
 US-08-553-257A-42

Query Match

Best Local Similarity

Matches

Score 34.1%; DB 2; Length 15;

Pred. No. 83.3%; Mismatches 0; Gaps 0; Indels 0;

Cl:

Qy 4 PSGAGG 9

|||

Db 9 FSGAGG 14

RESULT 13

US-09-441-992-42

Sequence 42, Application US/09441992

Patent No. 6541210

GENERAL INFORMATION:

APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA

MOLECOLARE P. ANGELUTTI S.P.A.

FELICI, Franco

LIZZAGO, Alessandra

NICOSIA, Alfredo

MONACI, Paolo

CORTESI, Riccardo

TITLE OF INVENTION:

PROCESS FOR THE PREPARATION OF IMMUNOGENS

OR IMMUNOGENS OR

DIAGNOSTIC REAGENTS THEREBY OBTAINABLE

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street N.W. Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: US

Z-P: 981C4-7092

COMPUTER READABLE FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,871C

FILING DATE: 02-MAY-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 24C052.4C9C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-5531
 TELEX: 3723836
 INFORMATION FOR SEQ ID NO: 91:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-43-871C-91

RESULT 15
 Query Match: 33.0%; Score 29; DB 2; Length 15;
 Best Local Similarity 45.5%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 APPLICANT: Loeb, Lawrence A.
 APPLICANT: Black, Margaret E.
 TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
 NUMBER OF SEQUENCES: 1C4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/270,956
 FILING DATE: 17-MAR-1999
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 24C052.4C9C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEX: 3723836
 INFORMATION FOR SEQ ID NO: 91:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-902-956-91

Query Match 33.0%; Score 29; DB 4; Length 15;
 Best Local Similarity 45.5%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 APPLICANT: Loeb, Lawrence A.
 APPLICANT: Black, Margaret E.
 TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
 NUMBER OF SEQUENCES: 1C4
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/270,956
 FILING DATE: 17-MAR-1999
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 24C052.4C9C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEX: 3723836
 INFORMATION FOR SEQ ID NO: 91:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-902-956-91